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14, 2006.**Publication Classification**(51) **Int. Cl.****A01H 1/00** (2006.01)**C07H 21/04** (2006.01)**C12N 15/82** (2006.01)**A01N 65/00** (2006.01)**C12N 5/04** (2006.01)(52) **U.S. Cl.** **800/279**; 435/419; 435/468;
530/350; 536/23.6; 514/12(57) **ABSTRACT**

Compositions and methods for conferring pesticidal activity to bacteria, plants, plant cells, tissues and seeds are provided. Compositions comprising a coding sequence for a delta-endotoxin polypeptide are provided. The coding sequences can be used in DNA constructs or expression cassettes for transformation and expression in plants and bacteria. Compositions also comprise transformed bacteria, plants, plant cells, tissues, and seeds. In particular, isolated delta-endotoxin nucleic acid molecules are provided. Additionally, amino acid sequences corresponding to the polynucleotides are encompassed, and antibodies specifically binding to those amino acid sequences. In particular, the present invention provides for isolated nucleic acid molecules comprising nucleotide sequences encoding the amino acid sequence shown in SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38, or the nucleotide sequence set forth in SEQ ID NO: 1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37, as well as variants and fragments thereof.

AXMI-031, AXMI-039, AXMI-040 AND AXMI-049, A FAMILY OF NOVEL DELTA ENDOTOXIN GENES AND METHODS FOR THEIR USE

CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of U.S. Provisional Application Serial No. 60/813,774, filed Jun. 14, 2006, the contents of which are herein incorporated by reference in their entirety.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0002] The official copy of the sequence listing is submitted electronically via EFS-Web as an ASCII formatted sequence listing with a file named "329212_SequenceListing.txt", created on Jun. 12, 2007, and having a size of 347 kilobytes and is filed concurrently with the specification. The sequence listing contained in this ASCII formatted document is part of the specification and is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0003] This invention relates to the field of molecular biology. Provided are novel genes that encode pesticidal proteins. These proteins and the nucleic acid sequences that encode them are useful in preparing pesticidal formulations and in the production of transgenic pest-resistant plants.

BACKGROUND OF THE INVENTION

[0004] *Bacillus thuringiensis* is a Gram-positive spore forming soil bacterium characterized by its ability to produce crystalline inclusions that are specifically toxic to certain orders and species of insects, but are harmless to plants and other non-targeted organisms. For this reason, compositions including *Bacillus thuringiensis* strains or their insecticidal proteins can be used as environmentally-acceptable insecticides to control agricultural insect pests or insect vectors for a variety of human or animal diseases.

[0005] Crystal (Cry) proteins (delta-endotoxins) from *Bacillus thuringiensis* have potent insecticidal activity against predominantly Lepidopteran, Dipteran, and Coleopteran larvae. These proteins also have shown activity against *Hymenoptera*, *Homoptera*, *Phthiraptera*, *Mallophaga*, and *Acari* pest orders, as well as other invertebrate orders such as *Nemathelminthes*, *Platyhelminthes*, and *Sarcomastigophora* (Feitelson (1993) The *Bacillus Thuringiensis* family tree. In *Advanced Engineered Pesticides*, Marcel Dekker, Inc., New York, N.Y.) These proteins were originally classified as CryI to CryV based primarily on their insecticidal activity. The major classes were *Lepidoptera*-specific (I), *Lepidoptera*- and *Diptera*-specific (II), *Coleoptera*-specific (III), *Diptera*-specific (IV), and nematode-specific (V) and (VI). The proteins were further classified into subfamilies; more highly related proteins within each family were assigned divisional letters such as CryIA, CryIB, CryIC, etc. Even more closely related proteins within each division were given names such as CryIC1, CryIC2, etc.

[0006] A new nomenclature was recently described for the Cry genes based upon amino acid sequence homology rather than insect target specificity (Crickmore et al. (1998) *Micro-*

biol. Mol. Biol. Rev. 62:807-813). In the new classification, each toxin is assigned a unique name incorporating a primary rank (an Arabic number), a secondary rank (an uppercase letter), a tertiary rank (a lowercase letter), and a quaternary rank (another Arabic number). In the new classification, Roman numerals have been exchanged for Arabic numerals in the primary rank. Proteins with less than 45% sequence identity have different primary ranks, and the criteria for secondary and tertiary ranks are 78% and 95%, respectively.

[0007] The crystal protein does not exhibit insecticidal activity until it has been ingested and solubilized in the insect midgut. The ingested protoxin is hydrolyzed by proteases in the insect digestive tract to an active toxic molecule. (Höfte and Whiteley (1989) *Microbiol. Rev.* 53:242-255). This toxin binds to apical brush border receptors in the midgut of the target larvae and inserts into the apical membrane creating ion channels or pores, resulting in larval death.

[0008] Delta-endotoxins generally have five conserved sequence domains, and three conserved structural domains (see, for example, de Maagd et al. (2001) *Trends Genetics* 17:193-199). The first conserved structural domain consists of seven alpha helices and is involved in membrane insertion and pore formation. Domain II consists of three beta-sheets arranged in a Greek key configuration, and domain III consists of two antiparallel beta-sheets in "jelly-roll" formation (de Maagd et al., 2001, *supra*). Domains II and III are involved in receptor recognition and binding, and are therefore considered determinants of toxin specificity.

[0009] Because of the devastation that insects can confer there is a continual need to discover new forms of *Bacillus thuringiensis* delta-endotoxins.

SUMMARY OF INVENTION

[0010] Compositions and methods for conferring pest resistance to bacteria, plants, plant cells, tissues and seeds are provided. Compositions include nucleic acid molecules encoding sequences for delta-endotoxin polypeptides, vectors comprising those nucleic acid molecules, and host cells comprising the vectors. Compositions also include the polypeptide sequences of the endotoxin, and antibodies to those polypeptides. The nucleotide sequences can be used in DNA constructs or expression cassettes for transformation and expression in organisms, including microorganisms and plants. The nucleotide or amino acid sequences may be synthetic sequences that have been designed for expression in an organism including, but not limited to, a microorganism or a plant. Compositions also comprise transformed bacteria, plants, plant cells, tissues, and seeds.

[0011] In particular, isolated nucleic acid molecules corresponding to delta-endotoxin nucleic acid sequences are provided. Additionally, amino acid sequences corresponding to the polynucleotides are encompassed. In particular, the present invention provides for an isolated nucleic acid molecule comprising a nucleotide sequence encoding the amino acid sequence shown in SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38, a nucleotide sequence set forth in SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37, or the delta-endotoxin nucleotide sequences deposited in bacterial hosts as Accession Nos. B-30935, B-30936, B-30937, and B-50046, as

well as variants and fragments thereof. Nucleotide sequences that are complementary to a nucleotide sequence of the invention, or that hybridize to a sequence of the invention are also encompassed.

[0012] Methods are provided for producing the polypeptides of the invention, and for using those polypeptides for controlling or killing a lepidopteran or coleopteran pest. Methods and kits for detecting the nucleic acids and polypeptides of the invention in a sample are also included.

[0013] Methods for controlling or killing a nematode pest population are further provided. The methods comprise introducing into a plant a polynucleotide encoding a nematode-active polypeptide with a molecular size greater than 22 kDa. These nematode-active polypeptides are useful for controlling or killing plant-parasitic nematodes, particularly cyst nematodes.

[0014] The compositions and methods of the invention are useful for the production of organisms with pesticide resistance, specifically bacteria and plants. These organisms and compositions derived from them are desirable for agricultural purposes. The compositions of the invention are also useful for generating altered or improved delta-endotoxin proteins that have pesticidal activity, or for detecting the presence of delta-endotoxin proteins or nucleic acids in products or organisms.

DETAILED DESCRIPTION

[0015] The present invention is drawn to compositions and methods for regulating pest resistance in organisms, particularly plants or plant cells. The methods involve transforming organisms with a nucleotide sequence encoding a delta-endotoxin protein of the invention. In particular, the nucleotide sequences of the invention are useful for preparing plants and microorganisms that possess pesticidal activity. Thus, transformed bacteria, plants, plant cells, plant tissues and seeds are provided. Compositions are delta-endotoxin nucleic acids and proteins of *Bacillus thuringiensis*. The sequences find use in the construction of expression vectors for subsequent transformation into organisms of interest, as probes for the isolation of other delta-endotoxin genes, and for the generation of altered pesticidal proteins by methods known in the art, such as domain swapping or DNA shuffling. The proteins find use in controlling or killing lepidopteran, coleopteran, and nematode pest populations, and for producing compositions with pesticidal activity.

[0016] Plasmids containing the nucleotide sequences of the invention were deposited in the permanent collection of the Agricultural Research Service Culture Collection, Northern Regional Research Laboratory (NRRL), 1815 North University Street, Peoria, Ill. 61604, United States of America, on Jun. 9, 2006, and assigned Accession Nos. NRRL B-30935 (for axmi-031), NRRL B-30936 (for axmi-039), and NRRL B-30937 (for axmi-040); and on May 29, 2007 and assigned NRRL B-50046 (axmi-049). These deposits will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. These deposits were made merely as a convenience for those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. § 112.

[0017] By “delta-endotoxin” is intended a toxin from *Bacillus thuringiensis* that has toxic activity against one or

more pests, including, but not limited to, members of the *Lepidoptera*, *Diptera*, and *Coleoptera* orders or members of the *Nematoda* phylum, or a protein that has homology to such a protein. In some cases, delta-endotoxin proteins have been isolated from other organisms, including *Clostridium bifermentans* and *Paenibacillus popilliae*. Delta-endotoxin proteins include amino acid sequences deduced from the full-length nucleotide sequences disclosed herein, and amino acid sequences that are shorter than the full-length sequences, either due to the use of an alternate downstream start site, or due to processing that produces a shorter protein having pesticidal activity. Processing may occur in the organism the protein is expressed in, or in the pest after ingestion of the protein. Delta-endotoxins include proteins identified as cry1 through cry43, cyt1 and cyt2, and Cyt-like toxin. There are currently over 250 known species of delta-endotoxins with a wide range of specificities and toxicities. For an expansive list see Crickmore et al. (1998), *Microbiol. Mol. Biol. Rev.* 62:807-813, and for regular updates see Crickmore et al. (2003) “*Bacillus thuringiensis* toxin nomenclature,” at www.biols.susx.ac.uk/Home/Neil_Crickmore/Bt/index.

[0018] Provided herein are novel isolated nucleotide sequences that confer pesticidal activity. Also provided are the amino acid sequences of the delta-endotoxin proteins. The protein resulting from translation of this gene allows cells to control or kill pests that ingest it.

Isolated Nucleic Acid Molecules, and Variants and Fragments Thereof

[0019] One aspect of the invention pertains to isolated or recombinant nucleic acid molecules comprising nucleotide sequences encoding delta-endotoxin proteins and polypeptides or biologically active portions thereof, as well as nucleic acid molecules sufficient for use as hybridization probes to identify delta-endotoxin encoding nucleic acids. As used herein, the term “nucleic acid molecule” is intended to include DNA molecules (e.g., recombinant DNA, cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

[0020] An “isolated” or “purified” nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. Preferably, an “isolated” nucleic acid is free of sequences (preferably protein encoding sequences) that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For purposes of the invention, “isolated” when used to refer to nucleic acid molecules excludes isolated chromosomes. For example, in various embodiments, the isolated delta-endotoxin encoding nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A delta-endotoxin protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of non-delta-endotoxin protein (also referred to herein as a “contaminating protein”).

[0021] Nucleotide sequences encoding the proteins of the present invention include the sequence set forth in SEQ ID NO:1, 3, 5, 34, and 37, the delta endotoxin nucleotide sequences deposited in bacterial hosts as Accession Nos. NRRL B-30935, B-30936, B-30937, and B-50046, and variants, fragments, and complements thereof (for example, SEQ ID NO:7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, and 32). By “complement” is intended a nucleotide sequence that is sufficiently complementary to a given nucleotide sequence such that it can hybridize to the given nucleotide sequence to thereby form a stable duplex. The corresponding amino acid sequence for the delta-endotoxin protein encoded by this nucleotide sequence are set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, and 37.

[0022] Nucleic acid molecules that are fragments of these delta-endotoxin encoding nucleotide sequences are also encompassed by the present invention (for example, SEQ ID NO:9, 11, 14, 18, 20, 22, and 24). By “fragment” is intended a portion of the nucleotide sequence encoding a delta-endotoxin protein. A fragment of a nucleotide sequence may encode a biologically active portion of a delta-endotoxin protein, or it may be a fragment that can be used as a hybridization probe or PCR primer using methods disclosed below. Nucleic acid molecules that are fragments of a delta-endotoxin nucleotide sequence comprise at least about 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2150, 2200, 2250, 2300, 2350, 2400, 2450, 2500, 2550, 2600, 2650, 2700, 2750, 2800, 2850, 2900, 2950, 3000, 3050, 3100, 3150, 3200, 3250, 3300, 3350 contiguous nucleotides, or up to the number of nucleotides present in a full-length delta-endotoxin encoding nucleotide sequence disclosed herein (for example, 3558 nucleotides for SEQ ID NO: 1, 3984 nucleotides for SEQ ID NO:3, 3720 nucleotides for SEQ ID NO:5, and 3669 nucleotides for SEQ ID NO:34) depending upon the intended use. By “contiguous” nucleotides is intended nucleotide residues that are immediately adjacent to one another. Fragments of the nucleotide sequences of the present invention will encode protein fragments that retain the biological activity of the delta-endotoxin protein and, hence, retain pesticidal activity. By “retains activity” is intended that the fragment will have at least about 30%, at least about 50%, at least about 70%, 80%, 90%, 95% or higher of the pesticidal activity of the delta-endotoxin protein. Methods for measuring pesticidal activity are well known in the art. See, for example, Czaplá and Lang (1990) *J. Econ. Entomol.* 83:2480-2485; Andrews et al. (1988) *Biochem. J.* 252:199-206; Marrone et al. (1985) *J. of Economic Entomology* 78:290-293; and U.S. Pat. No. 5,743,477, all of which are herein incorporated by reference in their entirety.

[0023] A fragment of a delta-endotoxin encoding nucleotide sequence that encodes a biologically active portion of a protein of the invention will encode at least about 15, 25, 30, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100 contiguous amino acids, or up to the total number of amino acids present in a full-length delta-endotoxin protein of the invention (for example, 1185 amino acids for SEQ ID NO:2, 1327 amino acids for SEQ ID NO:4, 1239 amino acids for SEQ ID NO:6, and 1223 amino acids for SEQ ID NO:35).

[0024] Preferred delta-endotoxin proteins of the present invention are encoded by a nucleotide sequence sufficiently identical to the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37. By “sufficiently identical” is intended an amino acid or nucleotide sequence that has at least about 60% or 65% sequence identity, about 70% or 75% sequence identity, about 80% or 85% sequence identity, about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater sequence identity compared to a reference sequence using one of the alignment programs described herein using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like.

[0025] To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., percent identity=number of identical positions/total number of positions (e.g., overlapping positions)×100). In one embodiment, the two sequences are the same length. The percent identity between two sequences can be determined using techniques similar to those described below, with or without allowing gaps. In calculating percent identity, typically exact matches are counted.

[0026] The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A nonlimiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (1990) *J. Mol. Biol.* 215:403. BLAST nucleotide searches can be performed with the BLASTN program, score=100, wordlength=12, to obtain nucleotide sequences homologous to delta-endotoxin-like nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTX program, score=50, wordlength=3, to obtain amino acid sequences homologous to delta-endotoxin protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al. (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al. (1997) *supra*. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) can be used. Alignment may also be performed manually by inspection.

[0027] Another non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the ClustalW algorithm (Higgins et al. (1994) *Nucleic Acids Res.* 22:4673-4680). ClustalW compares sequences and aligns the entirety of the amino acid or DNA sequence, and thus can provide data about the sequence conservation of the entire amino acid sequence. The ClustalW algorithm is used in several commercially available DNA/amino acid analysis software packages, such as the ALIGNX module of the

Vector NTI Program Suite (Invitrogen Corporation, Carlsbad, Calif.). After alignment of amino acid sequences with ClustalW, the percent amino acid identity can be assessed. A non-limiting example of a software program useful for analysis of ClustalW alignments is GENEDOC™. GENEDOC™ (Karl Nicholas) allows assessment of amino acid (or DNA) similarity and identity between multiple proteins. Another non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (1988) *CABIOS* 4: 11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0), which is part of the GCG Wisconsin Genetics Software Package, Version 10 (available from Accelrys, Inc., 9685 Scranton Rd., San Diego, Calif., USA). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

[0028] Unless otherwise stated, GAP Version 10, which uses the algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48(3):443-453, will be used to determine sequence identity or similarity using the following parameters: % identity and % similarity for a nucleotide sequence using GAP Weight of 50 and Length Weight of 3, and the nws-gapdna.cmp scoring matrix; % identity or % similarity for an amino acid sequence using GAP weight of 8 and length weight of 2, and the BLOSUM62 scoring program. Equivalent programs may also be used. By “equivalent program” is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by GAP Version 10.

[0029] The invention also encompasses variant nucleic acid molecules (for example, SEQ ID NO:7, 9, 11, 16, 18, 22, 24, 26, 28, 30, and 32). “Variants” of the delta-endotoxin encoding nucleotide sequences include those sequences that encode the delta-endotoxin proteins disclosed herein but that differ conservatively because of the degeneracy of the genetic code as well as those that are sufficiently identical as discussed above. Naturally occurring allelic variants can be identified with the use of well-known molecular biology techniques, such as polymerase chain reaction (PCR) and hybridization techniques as outlined below. Variant nucleotide sequences also include synthetically derived nucleotide sequences that have been generated, for example, by using site-directed mutagenesis but which still encode the delta-endotoxin proteins disclosed in the present invention as discussed below. Variant proteins encompassed by the present invention are biologically active, that is they continue to possess the desired biological activity of the native protein, that is, retaining pesticidal activity. By “retains activity” is intended that the variant will have at least about 30%, at least about 50%, at least about 70%, or at least about 80% of the pesticidal activity of the native protein. Methods for measuring pesticidal activity are well known in the art. See, for example, Czaplá and Lang (1990) *J. Econ. Entomol.* 83: 2480-2485; Andrews et al. (1988) *Biochem. J.* 252:199-206; Marrone et al. (1985) *J. of Economic Entomology* 78:290-293; and U.S. Pat. No. 5,743,477, all of which are herein incorporated by reference in their entirety.

[0030] The skilled artisan will further appreciate that changes can be introduced by mutation of the nucleotide sequences of the invention thereby leading to changes in the

amino acid sequence of the encoded delta-endotoxin proteins, without altering the biological activity of the proteins. Thus, variant isolated nucleic acid molecules can be created by introducing one or more nucleotide substitutions, additions, or deletions into the corresponding nucleotide sequence disclosed herein, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Such variant nucleotide sequences are also encompassed by the present invention.

[0031] For example, conservative amino acid substitutions may be made at one or more predicted, nonessential amino acid residues. A “nonessential” amino acid residue is a residue that can be altered from the wild-type sequence of a delta-endotoxin protein without altering the biological activity, whereas an “essential” amino acid residue is required for biological activity. A “conservative amino acid substitution” is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

[0032] Delta-endotoxins generally have five conserved sequence domains, and three conserved structural domains (see, for example, de Maagd et al. (2001) *Trends Genetics* 17:193-199). The first conserved structural domain consists of seven alpha helices and is involved in membrane insertion and pore formation. Domain II consists of three beta-sheets arranged in a Greek key configuration, and domain III consists of two antiparallel beta-sheets in “jelly-roll” formation (de Maagd et al., 2001, supra). Domains II and III are involved in receptor recognition and binding, and are therefore considered determinants of toxin specificity.

[0033] Amino acid substitutions may be made in nonconserved regions that retain function. In general, such substitutions would not be made for conserved amino acid residues, or for amino acid residues residing within a conserved motif, where such residues are essential for protein activity. Examples of residues that are conserved and that may be essential for protein activity include, for example, residues that are identical between all proteins contained in an alignment of the amino acid sequences of the present invention and known delta-endotoxin sequences. Examples of residues that are conserved but that may allow conservative amino acid substitutions and still retain activity include, for example, residues that have only conservative substitutions between all proteins contained in an alignment of the amino acid sequences of the present invention and known delta-endotoxin sequences. However, one of skill in the art would understand that functional variants may have minor conserved or nonconserved alterations in the conserved residues.

[0034] Alternatively, variant nucleotide sequences can be made by introducing mutations randomly along all or part of

the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ability to confer delta-endotoxin activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly, and the activity of the protein can be determined using standard assay techniques.

[0035] Using methods such as PCR, hybridization, and the like corresponding delta-endotoxin sequences can be identified, such sequences having substantial identity to the sequences of the invention. See, for example, Sambrook and Russell (2001) *Molecular Cloning: A Laboratory Manual*. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.) and Innis, et al. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, N.Y.).

[0036] In a hybridization method, all or part of the delta-endotoxin nucleotide sequence can be used to screen cDNA or genomic libraries. Methods for construction of such cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook and Russell, 2001, supra. The so-called hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker, such as other radioisotopes, a fluorescent compound, an enzyme, or an enzyme co-factor. Probes for hybridization can be made by labeling synthetic oligonucleotides based on the known delta-endotoxin-encoding nucleotide sequence disclosed herein. Degenerate primers designed on the basis of conserved nucleotides or amino acid residues in the nucleotide sequence or encoded amino acid sequence can additionally be used. The probe typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, at least about 25, at least about 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 consecutive nucleotides of delta-endotoxin encoding nucleotide sequence of the invention or a fragment or variant thereof. Methods for the preparation of probes for hybridization are generally known in the art and are disclosed in Sambrook and Russell, 2001, supra herein incorporated by reference.

[0037] For example, an entire delta-endotoxin sequence disclosed herein, or one or more portions thereof, may be used as a probe capable of specifically hybridizing to corresponding delta-endotoxin-like sequences and messenger RNAs. To achieve specific hybridization under a variety of conditions, such probes include sequences that are unique and are preferably at least about 10 nucleotides in length, or at least about 20 nucleotides in length. Such probes may be used to amplify corresponding delta-endotoxin sequences from a chosen organism by PCR. This technique may be used to isolate additional coding sequences from a desired organism or as a diagnostic assay to determine the presence of coding sequences in an organism. Hybridization techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, for example, Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

[0038] Hybridization of such sequences may be carried out under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which a probe will hybridize to its target sequence to a detectably greater degree than to other sequences (e.g., at

least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences that are 100% complementary to the probe can be identified (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, preferably less than 500 nucleotides in length.

[0039] Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C. for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37° C., and a wash in 1x to 2xSSC (20xSSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55° C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37° C., and a wash in 0.5x to 1xSSC at 55 to 60° C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.1xSSC at 60 to 65° C. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours.

[0040] Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (1984) *Anal. Biochem.* 138:267-284: $T_m = 81.5^\circ \text{C.} + 16.6 (\log M) + 0.41 (\% \text{ GC}) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, % GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1° C. for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to sequences of the desired identity. For example, if sequences with $\geq 90\%$ identity are sought, the T_m can be decreased 10° C. Generally, stringent conditions are selected to be about 5° C. lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4° C. lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10° C. lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20° C. lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a

T_m of less than 45° C. (aqueous solution) or 32° C. (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, N.Y.); and Ausubel et al., eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

Isolated Proteins and Variants and Fragments Thereof

[0041] Delta-endotoxin proteins are also encompassed within the present invention. By “delta-endotoxin protein” is intended a protein having the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38. Fragments, biologically active portions, and variants thereof are also provided, and may be used to practice the methods of the present invention.

[0042] “Fragments” or “biologically active portions” include polypeptide fragments comprising amino acid sequences sufficiently identical to the amino acid sequence set forth in SEQ ID NO:2, 4, 6, 8, 10, 12, 16, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38 and that exhibit pesticidal activity (for example, SEQ ID NO: 15, 19, 21, 23, or 25). A biologically active portion of a delta-endotoxin protein can be a polypeptide that is, for example, 10, 25, 50, 100 or more amino acids in length. Such biologically active portions can be prepared by recombinant techniques and evaluated for pesticidal activity. Methods for measuring pesticidal activity are well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.* 83:2480-2485; Andrews et al. (1988) *Biochem. J.* 252:199-206; Marrone et al. (1985) *J. of Economic Entomology* 78:290-293; and U.S. Pat. No. 5,743,477, all of which are herein incorporated by reference in their entirety. As used here, a fragment comprises at least 8 contiguous amino acids of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38. The invention encompasses other fragments, however, such as any fragment in the protein greater than about 10, 20, 30, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, or 1300 amino acids.

[0043] By “variants” is intended proteins or polypeptides having an amino acid sequence that is at least about 60%, 65%, about 70%, 75%, about 80%, 85%, about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 16, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38 (e.g., SEQ ID NO:10, 12, 17, 19, 23, 25, 27, 29, 31, or 33). Variants also include polypeptides encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule of SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37, or a complement thereof, under stringent conditions. Variants include polypeptides that differ in amino acid sequence due to mutagenesis. Variant proteins encompassed by the present invention are biologically active, that is they continue to possess the desired biological activity of the native protein, that is, retaining pesticidal activity. Methods for measuring pesticidal activity are well known in the art. See, for example, Czapla and Lang (1990) *J. Econ. Entomol.*

83:2480-2485; Andrews et al. (1988) *Biochem. J.* 252:199-206; Marrone et al. (1985) *J. of Economic Entomology* 78:290-293; and U.S. Pat. No. 5,743,477, all of which are herein incorporated by reference in their entirety.

[0044] Bacterial genes, such as the axmi-031, axmi-039, axmi-040, and axmi-049 genes of this invention, quite often possess multiple methionine initiation codons in proximity to the start of the open reading frame. Often, translation initiation at one or more of these start codons will lead to generation of a functional protein. These start codons can include ATG codons. However, bacteria such as *Bacillus sp.* also recognize the codon GTG as a start codon, and proteins that initiate translation at GTG codons contain a methionine at the first amino acid. Furthermore, it is not often determined a priori which of these codons are used naturally in the bacterium. Thus, it is understood that use of one of the alternate methionine codons may also lead to generation of delta-endotoxin proteins that encode pesticidal activity. These delta-endotoxin proteins are encompassed in the present invention and may be used in the methods of the present invention.

[0045] Antibodies to the polypeptides of the present invention, or to variants or fragments thereof, are also encompassed. Methods for producing antibodies are well known in the art (see, for example, Harlow and Lane (1988) *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.; U.S. Pat. No. 4,196,265).

Altered or Improved Variants

[0046] It is recognized that DNA sequences of a delta-endotoxin may be altered by various methods, and that these alterations may result in DNA sequences encoding proteins with amino acid sequences different than that encoded by a delta-endotoxin of the present invention. This protein may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions of one or more amino acids of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38, including up to about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, about 10, about 15, about 20, about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60, about 65, about 70, about 75, about 80, about 85, about 90, about 100, about 105, about 110, about 115, about 120, about 125, about 130 or more amino acid substitutions, deletions or insertions.

[0047] Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of a delta-endotoxin protein can be prepared by mutations in the DNA. This may also be accomplished by one of several forms of mutagenesis and/or in directed evolution. In some aspects, the changes encoded in the amino acid sequence will not substantially affect the function of the protein. Such variants will possess the desired pesticidal activity. However, it is understood that the ability of a delta-endotoxin to confer pesticidal activity may be improved by the use of such techniques upon the compositions of this invention. For example, one may express a delta-endotoxin in host cells that exhibit high rates of base misincorporation during DNA replication, such as XL-1 Red (Stratagene). After propagation in such strains, one can isolate the delta-endotoxin DNA (for example by preparing plasmid DNA, or by amplifying by PCR and cloning the resulting PCR fragment into a

vector), culture the delta-endotoxin mutations in a non-mutagenic strain, and identify mutated delta-endotoxin genes with pesticidal activity, for example by performing an assay to test for pesticidal activity. Generally, the protein is mixed and used in feeding assays. See, for example Marrone et al. (1985) *J. of Economic Entomology* 78:290-293. Such assays can include contacting plants with one or more pests and determining the plant's ability to survive and/or cause the death of the pests. Examples of mutations that result in increased toxicity are found in Schnepf et al. (1998) *Microbiol. Mol. Biol. Rev.* 62:775-806.

[0048] Alternatively, alterations may be made to the protein sequence of many proteins at the amino or carboxy terminus without substantially affecting activity. This can include insertions, deletions, or alterations introduced by modern molecular methods, such as PCR, including PCR amplifications that alter or extend the protein coding sequence by virtue of inclusion of amino acid encoding sequences in the oligonucleotides utilized in the PCR amplification. Alternatively, the protein sequences added can include entire protein-coding sequences, such as those used commonly in the art to generate protein fusions. Such fusion proteins are often used to (1) increase expression of a protein of interest (2) introduce a binding domain, enzymatic activity, or epitope to facilitate either protein purification, protein detection, or other experimental uses known in the art (3) target secretion or translation of a protein to a subcellular organelle, such as the periplasmic space of Gram-negative bacteria, or the endoplasmic reticulum of eukaryotic cells, the latter of which often results in glycosylation of the protein.

[0049] Variant nucleotide and amino acid sequences of the present invention also encompass sequences derived from mutagenic and recombinogenic procedures such as DNA shuffling. With such a procedure, one or more different delta-endotoxin protein coding regions can be used to create a new delta-endotoxin protein possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined in vitro or in vivo. For example, using this approach, sequence motifs encoding a domain of interest may be shuffled between a delta-endotoxin gene of the invention and other known delta-endotoxin genes to obtain a new gene coding for a protein with an improved property of interest, such as an increased insecticidal activity. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751; Stemmer (1994) *Nature* 370:389-391; Crameri et al. (1997) *Nature Biotech.* 15:436-438; Moore et al. (1997) *J. Mol. Biol.* 272:336-347; Zhang et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:4504-4509; Crameri et al. (1998) *Nature* 391:288-291; and U.S. Pat. Nos. 5,605,793 and 5,837,458.

[0050] Domain swapping or shuffling is another mechanism for generating altered delta-endotoxin proteins. Domains II and III may be swapped between delta-endotoxin proteins, resulting in hybrid or chimeric toxins with improved pesticidal activity or target spectrum. Methods for generating recombinant proteins and testing them for pesticidal activity are well known in the art (see, for example, Naimov et al. (2001) *Appl. Environ. Microbiol.* 67:5328-5330; de Maagd et al. (1996) *Appl. Environ. Microbiol.*

62:1537-1543; Ge et al. (1991) *J. Biol. Chem.* 266:17954-17958; Schnepf et al. (1990) *J. Biol. Chem.* 265:20923-20930; Rang et al. 91999) *Appl. Environ. Microbiol.* 65:2918-2925).

Vectors

[0051] A delta-endotoxin sequence of the invention may be provided in an expression cassette for expression in a plant of interest. By "plant expression cassette" is intended a DNA construct that is capable of resulting in the expression of a protein from an open reading frame in a plant cell. Typically these contain a promoter and a coding sequence. Often, such constructs will also contain a 3' untranslated region. Such constructs may contain a "signal sequence" or "leader sequence" (i.e., SEQ ID NO:9, 11, 28, 30, and 32) to facilitate co-translational or post-translational transport of the peptide to certain intracellular structures such as the chloroplast (or other plastid), endoplasmic reticulum, or Golgi apparatus.

[0052] By "signal sequence" is intended a sequence that is known or suspected to result in cotranslational or post-translational peptide transport across the cell membrane. In eukaryotes, this typically involves secretion into the Golgi apparatus, with some resulting glycosylation. By "leader sequence" is intended any sequence that when translated, results in an amino acid sequence (i.e., SEQ ID NO:10, 12, 29, 31, and 33) sufficient to trigger co-translational transport of the peptide chain to a sub-cellular organelle. Thus, this includes leader sequences targeting transport and/or glycosylation by passage into the endoplasmic reticulum, passage to vacuoles, plastids including chloroplasts, mitochondria, and the like.

[0053] By "plant transformation vector" is intended a DNA molecule that is necessary for efficient transformation of a plant cell. Such a molecule may consist of one or more plant expression cassettes, and may be organized into more than one "vector" DNA molecule. For example, binary vectors are plant transformation vectors that utilize two non-contiguous DNA vectors to encode all requisite cis- and trans-acting functions for transformation of plant cells (Hellen and Mullineaux (2000) *Trends in Plant Science* 5:446-451). "Vector" refers to a nucleic acid construct designed for transfer between different host cells. "Expression vector" refers to a vector that has the ability to incorporate, integrate and express heterologous DNA sequences or fragments in a foreign cell. The cassette will include 5' and 3' regulatory sequences operably linked to a sequence of the invention. By "operably linked" is intended a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame. The cassette may additionally contain at least one additional gene to be cotransformed into the organism. Alternatively, the additional gene(s) can be provided on multiple expression cassettes.

[0054] "Promoter" refers to a nucleic acid sequence that functions to direct transcription of a downstream coding sequence. The promoter together with other transcriptional and translational regulatory nucleic acid sequences (also termed "control sequences") are necessary for the expression of a DNA sequence of interest.

[0055] Such an expression cassette is provided with a plurality of restriction sites for insertion of the delta-endotoxin sequence to be under the transcriptional regulation of the regulatory regions.

[0056] The expression cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a DNA sequence of the invention, and a translational and transcriptional termination region (i.e., termination region) functional in plants. The promoter may be native or analogous, or foreign or heterologous, to the plant host and/or to the DNA sequence of the invention. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. Where the promoter is "native" or "homologous" to the plant host, it is intended that the promoter is found in the native plant into which the promoter is introduced. Where the promoter is "foreign" or "heterologous" to the DNA sequence of the invention, it is intended that the promoter is not the native or naturally occurring promoter for the operably linked DNA sequence of the invention.

[0057] The termination region may be native with the transcriptional initiation region, may be native with the operably linked DNA sequence of interest, may be native with the plant host, or may be derived from another source (i.e., foreign or heterologous to the promoter, the DNA sequence of interest, the plant host, or any combination thereof). Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau et al. (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon et al. (1991) *Genes Dev.* 5:141-149; Mogen et al. (1990) *Plant Cell* 2:1261-1272; Munroe et al. (1990) *Gene* 91:151-158; Ballas et al. (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi et al. (1987) *Nucleic Acid Res.* 15:9627-9639.

[0058] Where appropriate, the gene(s) may be optimized for increased expression in the transformed host cell. That is, the genes can be synthesized using host cell-preferred codons for improved expression, or may be synthesized using codons at a host-preferred codon usage frequency. Generally, the GC content of the gene will be increased. See, for example, Campbell and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of host-preferred codon usage. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Pat. Nos. 5,380,831, and 5,436,391, and Murray et al. (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

[0059] In one embodiment, the delta-endotoxin is targeted to the chloroplast for expression. In this manner, where the delta-endotoxin is not directly inserted into the chloroplast, the expression cassette will additionally contain a nucleic acid encoding a transit peptide to direct the delta-endotoxin to the chloroplasts. Such transit peptides are known in the art. See, for example, Von Heijne et al. (1991) *Plant Mol. Biol. Rep.* 9:104-126; Clark et al. (1989) *J. Biol. Chem.* 264:17544-17550; Della-Cioppa et al. (1987) *Plant Physiol.* 84:965-968; Romer et al. (1993) *Biochem. Biophys. Res. Commun.* 196:1414-1421; and Shah et al. (1986) *Science* 233:478-481.

[0060] The delta-endotoxin gene to be targeted to the chloroplast may be optimized for expression in the chloroplast to account for differences in codon usage between the

plant nucleus and this organelle. In this manner, the nucleic acids of interest may be synthesized using chloroplast-preferred codons. See, for example, U.S. Pat. No. 5,380,831, herein incorporated by reference.

Plant Transformation

[0061] Methods of the invention involve introducing a nucleotide construct into a plant. By "introducing" is intended to present to the plant the nucleotide construct in such a manner that the construct gains access to the interior of a cell of the plant. The methods of the invention do not require that a particular method for introducing a nucleotide construct to a plant is used, only that the nucleotide construct gains access to the interior of at least one cell of the plant. Methods for introducing nucleotide constructs into plants are known in the art including, but not limited to, stable transformation methods, transient transformation methods, and virus-mediated methods.

[0062] By "plant" is intended whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds, plant cells, propagules, embryos and progeny of the same. Plant cells can be differentiated or undifferentiated (e.g. callus, suspension culture cells, protoplasts, leaf cells, root cells, phloem cells, pollen).

[0063] "Transgenic plants" or "transformed plants" or "stably transformed" plants or cells or tissues refers to plants that have incorporated or integrated exogenous nucleic acid sequences or DNA fragments into the plant cell. These nucleic acid sequences include those that are exogenous, or not present in the untransformed plant cell, as well as those that may be endogenous, or present in the untransformed plant cell. "Heterologous" generally refers to the nucleic acid sequences that are not endogenous to the cell or part of the native genome in which they are present, and have been added to the cell by infection, transfection, microinjection, electroporation, microprojection, or the like.

[0064] Transformation of plant cells can be accomplished by one of several techniques known in the art. The delta-endotoxin gene of the invention may be modified to obtain or enhance expression in plant cells. Typically a construct that expresses such a protein would contain a promoter to drive transcription of the gene, as well as a 3' untranslated region to allow transcription termination and polyadenylation. The organization of such constructs is well known in the art. In some instances, it may be useful to engineer the gene such that the resulting peptide is secreted, or otherwise targeted within the plant cell. For example, the gene can be engineered to contain a signal peptide to facilitate transfer of the peptide to the endoplasmic reticulum. It may also be preferable to engineer the plant expression cassette to contain an intron, such that mRNA processing of the intron is required for expression.

[0065] Typically this "plant expression cassette" will be inserted into a "plant transformation vector". This plant transformation vector may be comprised of one or more DNA vectors needed for achieving plant transformation. For example, it is a common practice in the art to utilize plant transformation vectors that are comprised of more than one contiguous DNA segment. These vectors are often referred to in the art as "binary vectors". Binary vectors as well as vectors with helper plasmids are most often used for Agrobacterium-mediated transformation, where the size and

complexity of DNA segments needed to achieve efficient transformation is quite large, and it is advantageous to separate functions onto separate DNA molecules. Binary vectors typically contain a plasmid vector that contains the cis-acting sequences required for T-DNA transfer (such as left border and right border), a selectable marker that is engineered to be capable of expression in a plant cell, and a "gene of interest" (a gene engineered to be capable of expression in a plant cell for which generation of transgenic plants is desired). Also present on this plasmid vector are sequences required for bacterial replication. The cis-acting sequences are arranged in a fashion to allow efficient transfer into plant cells and expression therein. For example, the selectable marker gene and the delta-endotoxin are located between the left and right borders. Often a second plasmid vector contains the trans-acting factors that mediate T-DNA transfer from *Agrobacterium* to plant cells. This plasmid often contains the virulence functions (Vir genes) that allow infection of plant cells by *Agrobacterium*, and transfer of DNA by cleavage at border sequences and vir-mediated DNA transfer, as is understood in the art (Hellens and Mullineaux (2000) *Trends in Plant Science* 5:446-451). Several types of *Agrobacterium* strains (e.g. LBA4404, GV3101, EHA101, EHA105, etc.) can be used for plant transformation. The second plasmid vector is not necessary for transforming the plants by other methods such as microprojection, microinjection, electroporation, polyethylene glycol, etc.

[0066] In general, plant transformation methods involve transferring heterologous DNA into target plant cells (e.g. immature or mature embryos, suspension cultures, undifferentiated callus, protoplasts, etc.), followed by applying a maximum threshold level of appropriate selection (depending on the selectable marker gene) to recover the transformed plant cells from a group of untransformed cell mass. Explants are typically transferred to a fresh supply of the same medium and cultured routinely. Subsequently, the transformed cells are differentiated into shoots after placing on regeneration medium supplemented with a maximum threshold level of selecting agent. The shoots are then transferred to a selective rooting medium for recovering rooted shoot or plantlet. The transgenic plantlet then grows into a mature plant and produces fertile seeds (e.g. Hiei et al. (1994) *The Plant Journal* 6:271-282; Ishida et al. (1996) *Nature Biotechnology* 14:745-750). Explants are typically transferred to a fresh supply of the same medium and cultured routinely. A general description of the techniques and methods for generating transgenic plants are found in Ayres and Park (1994) *Critical Reviews in Plant Science* 13:219-239 and Bommineni and Jauhar (1997) *Maydica* 42:107-120. Since the transformed material contains many cells; both transformed and non-transformed cells are present in any piece of subjected target callus or tissue or group of cells. The ability to kill non-transformed cells and allow transformed cells to proliferate results in transformed plant cultures. Often, the ability to remove non-transformed cells is a limitation to rapid recovery of transformed plant cells and successful generation of transgenic plants.

[0067] Transformation protocols as well as protocols for introducing nucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Generation of transgenic plants may be performed by one of several methods, including, but not limited to, microinjection, electroporation, direct

gene transfer, introduction of heterologous DNA by *Agrobacterium* into plant cells (*Agrobacterium*-mediated transformation), bombardment of plant cells with heterologous foreign DNA adhered to particles, ballistic particle acceleration, aerosol beam transformation (U.S. Published Application No. 20010026941; U.S. Pat. No. 4,945,050; International Publication No. WO 91/00915; U.S. Published Application No. 2002015066), *Led1* transformation, and various other non-particle direct-mediated methods to transfer DNA.

[0068] Methods for transformation of chloroplasts are known in the art. See, for example, Svab et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:8526-8530; Svab and Maliga (1993) *Proc. Natl. Acad. Sci. USA* 90:913-917; Svab and Maliga (1993) *EMBO J.* 12:601-606. The method relies on particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by transactivation of a silent plastid-borne transgene by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:7301-7305.

[0069] Following integration of heterologous foreign DNA into plant cells, one then applies a maximum threshold level of appropriate selection in the medium to kill the untransformed cells and separate and proliferate the putatively transformed cells that survive from this selection treatment by transferring regularly to a fresh medium. By continuous passage and challenge with appropriate selection, one identifies and proliferates the cells that are transformed with the plasmid vector. Molecular and biochemical methods can then be used to confirm the presence of the integrated heterologous gene of interest into the genome of the transgenic plant.

[0070] The cells that have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick et al. (1986) *Plant Cell Reports* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having constitutive expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved. In this manner, the present invention provides transformed seed (also referred to as "transgenic seed") having a nucleotide construct of the invention, for example, an expression cassette of the invention, stably incorporated into their genome.

Evaluation of Plant Transformation

[0071] Following introduction of heterologous foreign DNA into plant cells, the transformation or integration of heterologous gene in the plant genome is confirmed by various methods such as analysis of nucleic acids, proteins and metabolites associated with the integrated gene.

[0072] PCR analysis is a rapid method to screen transformed cells, tissue or shoots for the presence of incorporated gene at the earlier stage before transplanting into the soil (Sambrook and Russell (2001) *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Laboratory Press,

Cold Spring Harbor, N.Y.). PCR is carried out using oligonucleotide primers specific to the gene of interest or *Agrobacterium* vector background, etc.

[0073] Plant transformation may be confirmed by Southern blot analysis of genomic DNA (Sambrook and Russell, 2001, *supra*). In general, total DNA is extracted from the transformant, digested with appropriate restriction enzymes, fractionated in an agarose gel and transferred to a nitrocellulose or nylon membrane. The membrane or "blot" is then probed with, for example, radiolabeled ^{32}P target DNA fragment to confirm the integration of introduced gene into the plant genome according to standard techniques (Sambrook and Russell, 2001, *supra*).

[0074] In Northern blot analysis, RNA is isolated from specific tissues of transformant, fractionated in a formaldehyde agarose gel, and blotted onto a nylon filter according to standard procedures that are routinely used in the art (Sambrook and Russell, 2001, *supra*). Expression of RNA encoded by the delta-endotoxin is then tested by hybridizing the filter to a radioactive probe derived from a delta-endotoxin, by methods known in the art (Sambrook and Russell, 2001, *supra*).

[0075] Western blot, biochemical assays and the like may be carried out on the transgenic plants to confirm the presence of protein encoded by the delta-endotoxin gene by standard procedures (Sambrook and Russell, 2001, *supra*) using antibodies that bind to one or more epitopes present on the delta-endotoxin protein.

Pesticidal Activity in Plants

[0076] In another aspect of the invention, one may generate transgenic plants expressing a delta-endotoxin that has pesticidal activity. Methods described above by way of example may be utilized to generate transgenic plants, but the manner in which the transgenic plant cells are generated is not critical to this invention. Methods known or described in the art such as *Agrobacterium*-mediated transformation, biolistic transformation, and non-particle-mediated methods may be used at the discretion of the experimenter. Plants expressing a delta-endotoxin may be isolated by common methods described in the art, for example by transformation of callus, selection of transformed callus, and regeneration of fertile plants from such transgenic callus. In such process, one may use any gene as a selectable marker so long as its expression in plant cells confers ability to identify or select for transformed cells.

[0077] A number of markers have been developed for use with plant cells, such as resistance to chloramphenicol, the aminoglycoside G418, hygromycin, or the like. Other genes that encode a product involved in chloroplast metabolism may also be used as selectable markers. For example, genes that provide resistance to plant herbicides such as glyphosate, bromoxynil, or imidazolinone may find particular use. Such genes have been reported (Stalker et al. (1985) *J. Biol. Chem.* 263:6310-6314 (bromoxynil resistance nitrilase gene); and Sathasivan et al. (1990) *Nucl. Acids Res.* 18:2188 (AHAS imidazolinone resistance gene). Additionally, the genes disclosed herein are useful as markers to assess transformation of bacterial or plant cells. Methods for detecting the presence of a transgene in a plant, plant organ (e.g., leaves, stems, roots, etc.), seed, plant cell, propagule, embryo or progeny of the same are well known in the art. In

one embodiment, the presence of the transgene is detected by testing for pesticidal activity.

[0078] Fertile plants expressing a delta-endotoxin may be tested for pesticidal activity, and the plants showing optimal activity selected for further breeding. Methods are available in the art to assay for pest activity. Generally, the protein is mixed and used in feeding assays. See, for example Marrone et al. (1985) *J. of Economic Entomology* 78:290-293.

[0079] The present invention may be used for transformation of any plant species, including, but not limited to, monocots and dicots. Examples of plants of interest include, but are not limited to, corn (maize), sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, and oilseed rape, *Brassica* sp., alfalfa, rye, millet, safflower, peanuts, sweet potato, cassava, coffee, coconut, pineapple, citrus trees, cocoa, tea, banana, avocado, fig, guava, mango, olive, papaya, cashew, macadamia, almond, oats, vegetables, ornamentals, and conifers.

[0080] Vegetables include, but are not limited to, tomatoes, lettuce, green beans, lima beans, peas, and members of the genus *Curcumis* such as cucumber, cantaloupe, and musk melon. Ornamentals include, but are not limited to, azalea, hydrangea, hibiscus, roses, tulips, daffodils, petunias, carnation, poinsettia, and chrysanthemum. Preferably, plants of the present invention are crop plants (for example, maize, sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, oilseed rape, etc.).

Use in Pest Control

[0081] General methods for employing strains comprising a nucleotide sequence of the present invention, or a variant thereof, in pesticide control or in engineering other organisms as pesticidal agents are known in the art. See, for example U.S. Pat. No. 5,039,523 and EP 0480762A2.

[0082] The *Bacillus* strains containing a nucleotide sequence of the present invention, or a variant thereof, or the microorganisms that have been genetically altered to contain a pesticidal gene and protein may be used for protecting agricultural crops and products from pests. In one aspect of the invention, whole, i.e., unlysed, cells of a toxin (pesticide)-producing organism are treated with reagents that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s).

[0083] Alternatively, the pesticide is produced by introducing a delta-endotoxin gene into a cellular host. Expression of the delta-endotoxin gene results, directly or indirectly, in the intracellular production and maintenance of the pesticide. In one aspect of this invention, these cells are then treated under conditions that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s). The resulting product retains the toxicity of the toxin. These naturally encapsulated pesticides may then be formulated in accordance with conventional techniques for application to the environment hosting a target pest, e.g., soil, water, and foliage of plants. See, for example EPA 0192319, and the references cited therein. Alternatively, one may formulate the cells expressing a gene of this invention such as to allow application of the resulting material as a pesticide.

[0084] Nematode Control

[0085] Plant-parasitic nematodes, including cyst nematodes, root knot nematodes, and other nematodes, cause billions of dollars in damage to crops every year. Plant-parasitic nematodes pierce plant cell walls with their stylet, which is formed by some of the mouth and esophagus parts, and pump up the plant cell just into their digestive system. Numerous publications in the art conclude that sedentary plant parasitic nematodes do not ingest molecules larger than about 23-28 kDa in vivo. This has led to the widespread belief that the feeding tube produced by these nematodes acts as a molecular sieve, restricting the size of molecules that can be ingested. Bockenhoff and Grundler ((1994) *Parasitology* 109:249-254) injected fluorescently labeled dextrans into syncytia that were being fed upon by *Heterodera schachtii*. They found that the nematodes ingested 22 kDa dextrans, but not 40 kDa dextrans. Urwin et al. ((1998) *Planta* 204:472-479) found that a 23 kDa fusion protein expressed in transgenic *Arabidopsis* could not be ingested by *H. schachtii*, although a protein of about 11 kDa could be ingested. Similarly, Unwin et al. ((1997) *Molecular Plant-Microbe Interactions* 10:394-400) found that 28 kDa green fluorescent protein (GFP) expressed in transgenic *Arabidopsis* could not be ingested by *H. schachtii*. Thus, it was not previously recognized or demonstrated that nematodes could be controlled by expressing a protein greater than 22 kDa in a plant since it was understood that nematodes would not ingest such a protein.

[0086] Provided herein are methods and compositions for conferring resistance to nematodes in plants. The methods comprise introducing into a plant at least one nucleotide sequence encoding a nematode-active polypeptide and growing the plant in a field containing nematodes. By "nematode-active polypeptide" is intended a polypeptide that, when ingested by the nematode, results in the death or stunting of growth or proliferation of at least one nematode. In one embodiment, the nematode-active polypeptide has a molecular weight greater than about 22 kDa, about 23 kDa, about 24, about 25, about 26, about 27, about 28, about 29, about 30, about 31, about 32, about 33, about 34, about 35, about 36, about 37, about 38, about 39, about 40, about 41, about 42, about 43, about 44, about 45, about 46, about 47, about 48, about 49, about 50, about 51, about 52, about 53, about 54, about 55, about 56, about 57, about 58, about 59, about 60, about 61, about 62, about 63, about 64, about 65, about 66, about 67, about 68, about 69, about 70, about 71, about 72, about 73, about 74, about 75, about 76, about 77, about 78, about 79, about 80 kDa, or greater.

[0087] In another embodiment, the nematode-active polypeptide has activity against plant-parasitic nematodes. Expression of the nematode-active polypeptide in a plant reduces the ability of nematodes to infest or feed on roots of the plant. Examples of plant-parasitic nematodes sensitive to the compositions of the present invention include root knot nematodes (*Meloidogyne* sp.), stunt nematode (*Tylenchorynchus* sp.), lance nematode (*Hoplolaimus* sp.), spiral nematode (*Helicotylenchus* sp.), lesion nematode (*Pratylenchus* sp.), cyst nematode (*Heterodera* sp. and *Globodera* sp.), and ring nematode (*Criconea* sp.).

[0088] Pesticidal Compositions

[0089] The active ingredients of the present invention are normally applied in the form of compositions and can be

applied to the crop area or plant to be treated, simultaneously or in succession, with other compounds. These compounds can be fertilizers, weed killers, cryoprotectants, surfactants, detergents, pesticidal soaps, dormant oils, polymers, and/or time-release or biodegradable carrier formulations that permit long-term dosing of a target area following a single application of the formulation. They can also be selective herbicides, chemical insecticides, virucides, microbicides, amoebicides, pesticides, fungicides, bacteriocides, nematocides, molluscicides or mixtures of several of these preparations, if desired, together with further agriculturally acceptable carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g. natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders or fertilizers. Likewise the formulations may be prepared into edible "baits" or fashioned into pest "traps" to permit feeding or ingestion by a target pest of the pesticidal formulation.

[0090] Methods of applying an active ingredient of the present invention or an agrochemical composition of the present invention that contains at least one of the pesticidal proteins produced by the bacterial strains of the present invention include leaf application, seed coating and soil application. The number of applications and the rate of application depend on the intensity of infestation by the corresponding pest.

[0091] The composition may be formulated as a powder, dust, pellet, granule, spray, emulsion, colloid, solution, or such like, and may be prepared by such conventional means as desiccation, lyophilization, homogenation, extraction, filtration, centrifugation, sedimentation, or concentration of a culture of cells comprising the polypeptide. In all such compositions that contain at least one such pesticidal polypeptide, the polypeptide may be present in a concentration of from about 1% to about 99% by weight.

[0092] Lepidopteran, coleopteran, or nematode pests may be killed or reduced in numbers in a given area by the methods of the invention, or may be prophylactically applied to an environmental area to prevent infestation by a susceptible pest. Preferably the pest ingests, or is contacted with, a pesticidally-effective amount of the polypeptide. By "pesticidally-effective amount" is intended an amount of the pesticide that is able to bring about death to at least one pest, or to noticeably reduce pest growth, feeding, or normal physiological development. This amount will vary depending on such factors as, for example, the specific target pests to be controlled, the specific environment, location, plant, crop, or agricultural site to be treated, the environmental conditions, and the method, rate, concentration, stability, and quantity of application of the pesticidally-effective polypeptide composition. The formulations may also vary with respect to climatic conditions, environmental considerations, and/or frequency of application and/or severity of pest infestation.

[0093] The pesticide compositions described may be made by formulating either the bacterial cell, crystal and/or spore suspension, or isolated protein component with the desired agriculturally-acceptable carrier. The compositions may be formulated prior to administration in an appropriate means

such as lyophilized, freeze-dried, desiccated, or in an aqueous carrier, medium or suitable diluent, such as saline or other buffer. The formulated compositions may be in the form of a dust or granular material, or a suspension in oil (vegetable or mineral), or water or oil/water emulsions, or as a wettable powder, or in combination with any other carrier material suitable for agricultural application. Suitable agricultural carriers can be solid or liquid and are well known in the art. The term "agriculturally-acceptable carrier" covers all adjuvants, inert components, dispersants, surfactants, tackifiers, binders, etc. that are ordinarily used in pesticide formulation technology; these are well known to those skilled in pesticide formulation. The formulations may be mixed with one or more solid or liquid adjuvants and prepared by various means, e.g., by homogeneously mixing, blending and/or grinding the pesticidal composition with suitable adjuvants using conventional formulation techniques. Suitable formulations and application methods are described in U.S. Pat. No. 6,468,523, herein incorporated by reference.

[0094] "Pest" includes but is not limited to, insects, fungi, bacteria, nematodes, mites, ticks, and the like. Insect pests include insects selected from the orders *Coleoptera*, *Diptera*, *Hymenoptera*, *Lepidoptera*, *Mallophaga*, *Homoptera*, *Hemiptera*, *Orthoptera*, *Thysanoptera*, *Dermoptera*, *Isoptera*, *Anoplura*, *Siphonaptera*, *Trichoptera*, etc., particularly *Coleoptera*, *Lepidoptera*, and *Diptera*.

[0095] The order *Coleoptera* includes the suborders *Adephaga* and *Polyphaga*. Suborder *Adephaga* includes the superfamilies *Caraboidea* and *Gyrinoidea*, while suborder *Polyphaga* includes the superfamilies *Hydrophiloidea*, *Staphylinoidea*, *Cantharoidea*, *Clerioidea*, *Elateroidea*, *Dascilloidea*, *Dryopoidea*, *Byrrhoidea*, *Cucujoidea*, *Meloidea*, *Mordelloidea*, *Tenebrionoidea*, *Bostrichoidea*, *Scarabaeoidea*, *Cerambycoidea*, *Chrysomeloidea*, and *Curculionioidea*. Superfamily *Caraboidea* includes the families *Cicindelidae*, *Carabidae*, and *Dytiscidae*. Superfamily *Gyrinoidea* includes the family *Gyrinidae*. Superfamily *Hydrophiloidea* includes the family *Hydrophilidae*. Superfamily *Staphylinoidea* includes the families *Silphidae* and *Staphylinidae*. Superfamily *Cantharoidea* includes the families *Cantharidae* and *Lampyridae*. Superfamily *Clerioidea* includes the families *Cleridae* and *Dermestidae*. Superfamily *Elateroidea* includes the families *Elateridae* and *Buprestidae*. Superfamily *Cucujoidea* includes the family *Coccinellidae*. Superfamily *Meloidea* includes the family *Meloidae*. Superfamily *Tenebrionoidea* includes the family *Tenebrionidae*. Superfamily *Scarabaeoidea* includes the families *Passalidae* and *Scarabaeidae*. Superfamily *Cerambycoidea* includes the family *Cerambycidae*. Superfamily *Chrysomeloidea* includes the family *Chrysomelidae*. Superfamily *Curculionioidea* includes the families *Curculionidae* and *Scolytidae*.

[0096] The order *Diptera* includes the Suborders *Nematocera*, *Brachycera*, and *Cyclorrhapha*. Suborder *Nematocera* includes the families *Tipulidae*, *Psychodidae*, *Culicidae*, *Ceratopogonidae*, *Chironomidae*, *Simuliidae*, *Bibionidae*, and *Cecidomyiidae*. Suborder *Brachycera* includes the families *Stratiomyidae*, *Tabanidae*, *Therevidae*, *Asilidae*, *Mydidae*, *Bombyliidae*, and *Dolichopodidae*. Suborder *Cyclorrhapha* includes the Divisions *Aschiza* and *Aschiza*. Division *Aschiza* includes the families *Phoridae*, *Syrphidae*, and *Conopidae*. Division *Aschiza* includes the

Sections *Acalypterae* and *Calypterae*. Section *Acalypterae* includes the families *Otitidae*, *Tephritidae*, *Agromyzidae*, and *Drosophilidae*. Section *Calypterae* includes the families *Hippoboscidae*, *Oestridae*, *Tachinidae*, *Anthomyiidae*, *Muscidae*, *Calliphoridae*, and *Sarcophagidae*.

[0097] The order *Lepidoptera* includes the families *Papilionidae*, *Pieridae*, *Lycaenidae*, *Nymphalidae*, *Danaidae*, *Satyridae*, *Hesperiidae*, *Sphingidae*, *Saturniidae*, *Geometridae*, *Arctiidae*, *Noctuidae*, *Lymantriidae*, *Sesiidae*, and *Tineidae*.

[0098] Insect pests of the invention for the major crops include: Maize: *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Helicoverpa zea*, corn earworm; *Spodoptera frugiperda*, fall armyworm; *Diatraea grandiosella*, southwestern corn borer; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Diatraea saccharalis*, sugarcane borer; *Diabrotica virgifera*, western corn rootworm; *Diabrotica longicornis barberi*, northern corn rootworm; *Diabrotica undecimpunctata howardi*, southern corn rootworm; *Melanotus* spp., wireworms; *Cyclocephala borealis*, northern masked chafer (white grub); *Cyclocephala immaculata*, southern masked chafer (white grub); *Popillia japonica*, Japanese beetle; *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*, corn leaf aphid; *Anuraphis maidiradicis*, corn root aphid; *Blissus leucopterus leucopterus*, chinch bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Hylemya platura*, seedcorn maggot; *Agromyza parvicornis*, corn blot leafminer; *Anaphothrips obscurus*, grass thrips; *Solenopsis milesta*, thief ant; *Tetranychus urticae*, twospotted spider mite; Sorghum: *Chilo partellus*, sorghum borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Feltia subterranea*, granulate cutworm; *Phyllophaga crinita*, white grub; *Eleodes*, *Conoderus*, and *Aeolus* spp., wireworms; *Oulema melanopus*, cereal leaf beetle; *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*, corn leaf aphid; *Sipha flava*, yellow sugarcane aphid; *Blissus leucopterus leucopterus*, chinch bug; *Contarinia sorghicola*, sorghum midge; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, twospotted spider mite; Wheat: *Pseudaleia unipunctata*, army worm; *Spodoptera frugiperda*, fall armyworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Agrotis orthogonia*, western cutworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Oulema melanopus*, cereal leaf beetle; *Hypera punctata*, clover leaf weevil; *Diabrotica undecimpunctata howardi*, southern corn rootworm; Russian wheat aphid; *Schizaphis graminum*, greenbug; *Macrosiphum avenae*, English grain aphid; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Mayetiola destructor*, Hessian fly; *Sitodiplosis mosellana*, wheat midge; *Meromyza americana*, wheat stem maggot; *Hylemya coarctata*, wheat bulb fly; *Frankliniella fusca*, tobacco thrips; *Cephus cinctus*, wheat stem sawfly; *Aceria tulipae*, wheat curl mite; Sunflower: *Suleima helianthana*, sunflower bud moth; *Homoeosoma electellum*, sunflower moth; zygogramma exclamationis, sunflower beetle; *Bothyrus gibbosus*, carrot beetle; *Neolasioptera murtfeldiana*, sunflower seed midge; Cotton: *Heliothis virescens*, cotton budworm; *Helicoverpa zea*, cotton bollworm; *Spodoptera exigua*, beet armyworm; *Pectino-*

phora gossypiella, pink bollworm; *Anthonomus grandis*, boll weevil; *Aphis gossypii*, cotton aphid; *Pseudatoscelis seriatus*, cotton fleahopper; *Trialeurodes abutilonea*, band-winged whitefly; *Lygus lineolaris*, tarnished plant bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Thrips tabaci*, onion thrips; *Frankliniella fusca*, tobacco thrips; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, twospotted spider mite; Rice: *Diatraea saccharalis*, sugarcane borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Colaspis brunnea*, grape colaspis; *Lissorhoptus oryzophilus*, rice water weevil; *Sitophilus oryzae*, rice weevil; *Nephotettix nigropictus*, rice leafhopper; *Blissus leucopterus leucopterus*, chinch bug; *Acrosternum hilare*, green stink bug; Soybean: *Pseudoplusia includens*, soybean looper; *Anticarsia gemmatilis*, velvet-bean caterpillar; *Plathypena scabra*, green cloverworm; *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Spodoptera exigua*, beet armyworm; *Heliothis virescens*, cotton budworm; *Helicoverpa zea*, cotton bollworm; *Epilachna varivestis*, Mexican bean beetle; *Myzus persicae*, green peach aphid; *Empoasca fabae*, potato leafhopper; *Acrosternum hilare*, green stink bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Hylemya platura*, seed-corn maggot; *Sericothrips variabilis*, soybean thrips; *Thrips tabaci*, onion thrips; *Tetranychus turkestanii*, strawberry spider mite; *Tetranychus urticae*, twospotted spider mite; Barley: *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Schizaphis graminum*, greenbug; *Blissus leucopterus leucopterus*, chinch bug; *Acrosternum hilare*, green stink bug; *Euschistus servus*, brown stink bug; *Delia platura*, seedcorn maggot; *Mayetiola destructor*, Hessian fly; *Petrobia latens*, brown wheat mite; Oil Seed Rape: *Brevicoryne brassicae*, cabbage aphid; *Phyllotreta cruciferae*, Flea beetle; *Mamestra configurata*, Bertha armyworm; *Plutella xylostella*, Diamond-back moth; *Delia* spp., Root maggots.

[0099] Nematodes include parasitic nematodes such as root-knot, cyst, and lesion nematodes, including *Heterodera* spp., *Meloidogyne* spp., and *Globodera* spp.; particularly members of the cyst nematodes, including, but not limited to, *Heterodera glycines* (soybean cyst nematode); *Heterodera schachtii* (beet cyst nematode); *Heterodera avenae* (cereal cyst nematode); and *Globodera rostochiensis* and *Globodera pailida* (potato cyst nematodes). Lesion nematodes include *Pratylenchus* spp.

Methods for Increasing Plant Yield

[0100] Methods for increasing plant yield are provided. The methods comprise introducing into a plant or plant cell a polynucleotide comprising a pesticidal sequence disclosed herein. As defined herein, the "yield" of the plant refers to the quality and/or quantity of biomass produced by the plant. By "biomass" is intended any measured plant product. An increase in biomass production is any improvement in the yield of the measured plant product. Increasing plant yield has several commercial applications. For example, increasing plant leaf biomass may increase the yield of leafy vegetables for human or animal consumption. Additionally, increasing leaf biomass can be used to increase production of plant-derived pharmaceutical or industrial products. An increase in yield can comprise any statistically significant increase including, but not limited to, at least a 1% increase,

at least a 3% increase, at least a 5% increase, at least a 10% increase, at least a 20% increase, at least a 30%, at least a 50%, at least a 70%, at least a 100% or a greater increase in yield compared to a plant not expressing the pesticidal sequence.

[0101] In specific methods, plant yield is increased as a result of improved pest resistance of a plant expressing a pesticidal protein disclosed herein. Expression of the pesticidal protein results in a reduced ability of a pest to infest or feed on the plant, thus improving plant yield.

[0102] The following examples are offered by way of illustration and not by way of limitation.

EXPERIMENTAL

Example 1

Growth of ATX9387, and Preparation of Extracts

[0103] Strain ATX9387, identified as a member of the *Bacillus cereus*/*Bacillus thuringiensis* group by MIDI analysis, was grown in T3 medium at 30 degrees for times ranging from 16 hours to 5 days. Cultures were centrifuged and the supernatants were passed through 0.2 micron filters, resulting in sterile supernatants

Example 2

C. elegans bioassay

[0104] *Caenorhabditis elegans* ("C. elegans") hermaphrodites were reared as known in the art, to generate populations of healthy animals for bioassay. General procedures for growth, harvesting, and genetic manipulation of C elegans including growth media, etc. may be found in the art, for example, in Wood, ed. (1988) *The Nematode Caenorhabditis elegans* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

[0105] Sterile supernatants from strain ATX9387 were tested for activity on *C. elegans*. Bioassays were performed in 96-well plates. Five to ten nematodes were added to 80 μ l of S medium (Wood, supra) and were mixed with 20 μ l of sterile supernatant, 0.5 μ l of concentrated HB101 (prepared as described in Wood, supra) and rifampicin (final concentration of 0.1 μ g/ μ l). Assays were allowed to proceed at room temperature for 3 days and nematodes were quantitated. Negative control samples (T3 medium or sterile supernatants from inactive strains) contained hundreds of active nematodes, while test samples (containing ATX9387 supernatant) contained 5 to 10 nematodes that were sluggish or dead. The results of the bioassay of ATX9387 extracts on *C. elegans* are shown in Table 1.

TABLE 1

Activity of ATX9387 extracts on <i>C. elegans</i>		
Growth Time	ATX9387	Control
16 hours	—	—
1 day	—	—
2 days	—	—
3 days	++	—
4 days	++	—
5 days	++	—

Example 3

Activity of ATX9387 on Soybean Cyst Nematodes

[0106] A sterile supernatant of a 5-day culture of ATX9387 was concentrated 40-fold and fed to SCN J2 nematodes. Nematodes feeding on sterile supernatant were reproducibly observed to be sluggish, and exhibited higher motility than nematodes fed extract of a negative control concentrated to the same extent.

Example 4

Anti-nematode Activity from ATX9387 is Conferred by a Protein

[0107] To identify the anti-nematode activity in ATX9387, the following tests were performed. First, the ability of the activity to be destroyed by heating was tested by heating samples of sterile supernatant from ATX9387 to 100° C. for 10 minutes, then assaying heated material in a nematode bioassay. Heat treatment of sterile supernatants from ATX9387 resulted in a loss of anti-nematode activity. Next, active samples were treated with pronase to degrade proteins. This treatment resulted in loss of activity. Sterile supernatants from ATX9387 were passed through a 3 kDa molecular weight cut-off ("MWCO") concentration unit. The active ingredient was retained by the 3 kDa MWCO filter while the flow-through showed no activity. This indicates that the active molecule was larger than 3 kDa in size.

Example 5

Fractionation of Activity from ATX9387

[0108] The sterile supernatant of a 4-day culture of ATX9387 was fractionated by liquid chromatography on an anion exchange column in 20 mM Tris pH 8, using a gradient from 0 M to 1 M NaCl. Several consecutive fractions were active. The most active fraction was subjected to SDS-PAGE, and two prominent bands of approximately 130 kd and approximately 70 kd were observed.

[0109] In another experiment strain ATX9387 was grown for 5 days in T3 medium at 30° C. The culture was centrifuged at 8,000×g for 10 minutes, and the supernatant was passed through a 0.2 µm filter. The filtered supernatant was dialyzed against 20 mM Tris pH 8 using Spectra/Por 1 dialysis tubing (6-8,000 MWCO), and was then fractionated on an anion exchange column (Mono Q) using a gradient from 0 to 1 M NaCl over 20 bed volumes. The fractions were dialyzed against 20 mM Tris pH 8 using Slide-A-Lyzer (Pierce Biotechnology, Rockford, Ill.) mini dialysis units (7,000 MWCO), and bioassayed on *C. elegans* using 20 µl of sample in a 100 µl bioassay volume, as described herein. Fractions 12 and 13 were found to be active, and were pooled and then concentrated 7-fold using an Amicon Ultra-4 5,000 MWCO concentrator. The concentrated material was fractionated on a gel filtration column (Superdex 200) in 50 mM sodium phosphate, 150 mM NaCl, pH 7. Fractions were concentrated 10-fold using Centricon YM-3 concentrators, and were bioassayed on *C. elegans* as above. Fractions 5 and 6 were the most active, and fraction 7 was somewhat active. SDS-PAGE of the fractions showed that fractions 5-7 shared several proteins: a protein at about 130 kDa, a doublet at about 75 kDa, and a protein at about 53 kDa. The most prominent bands were subjected to N-termi-

nal protein sequencing by Edman degradation. The 130 kDa protein and the 70 kDa protein had very similar N-terminal sequences (cysteine could not be detected by the method used), and thus are likely to result from the same initial protein. This protein was designated as AXMI-031 (SEQ ID NO:2).

TABLE 2

N-terminal sequence of the ~130 kDa protein from ATX9387

1	A, S + S', M
2	D, Q
3	?, P, N
4	N
5	L
6	Q
7	S
8	Q
9	?, Q
10	N
11	I
12	P
13	Y
14	N
15	V

[0110]

TABLE 3

N-terminal sequence of the about ~70 kDa protein from ATX9387

1	A, G, S + S'
2	F
3	P
4	N
5	L
6	Q
7	V?
8	Q
9	?
10	N?, V?
11	I
12	P
13	Y, Q
14	?, N
15	?, V

A search of protein databases with the N-terminal sequences of the ~130 kDa protein and the ~70 kDa protein demonstrated that the N-terminal amino acids of the AXMI-031 proteins have significant similarity to the N-terminus of the endotoxin Cry14Aa (SEQ ID NO:13).

[0111] N-terminal sequence of Cry14A: MDCN-LQSQQNIPYNV (amino acid residues 1 through 15 of SEQ ID NO:13).

Example 6

Cloning of the axmi-031 Coding Region from ATX9387.

[0112] A random fragment library of ATX9387 was generated, and a DNA clone (pAX031) containing the DNA sequence encoding the N-terminus of axmi-031 was identified. A second clone, pAX032, was identified as containing the C-terminus of axmi-031. Clones pAX031 and pAX032 overlap substantially, such that it is clear to one skilled in the art that both clones together comprise the entire axmi-031 coding region.

[0113] To confirm the nature of the AXMI-031, a genomic clone was amplified using a high fidelity polymerase PFU ULTRA™ (Stratagene) from total DNA using primers designed to the ends of the axmi-031 open reading frame. The resulting PCR product was cloned into the PCR-TOPOII-Blunt vector (Invitrogen) to create pAX980. The DNA sequence pAX980 was determined and found to contain the same open reading frame as in the random fragment library clones pAX031 and pAX032. Translation of this open reading frame generates a protein sequence consistent with the N-terminal sequence obtained from the purified AXMI-031 protein. Thus, this open reading frame was designated axmi-031 (SEQ ID NO:1). The plasmid clone pAX2515, containing axmi-031 was deposited on Jun. 9, 2006 and assigned the accession number NRRL B-30935.

Example 7

Comparison of AXMI-031 to Other Known Endotoxins

[0114] Database searches using the AXMI-031 protein sequence demonstrate that AXMI-031 is a member of the delta-endotoxin class of insecticidal proteins. AXMI-031 is most similar to the cry14Aa endotoxin. The amino acid sequence of AXMI-031 is 86.6% identical to CRY14Aa (SEQ ID NO:13).

Example 8

Expression of the AXMI-031 Polypeptide in *E. coli*

[0115] For soluble expression in *E. coli*, primers were designed to include the translation start and stop codons from the axmi-031 ORF. The primers added an optimal RBS and Gateway attB recombination sites. Stratagene Pfu I polymerase was used to consistently amplify the ORF from the pAX980, and recombined with pDONR221 (Invitrogen, Carlsbad, Calif.) to create the entry vector pAX2515 (as per protocols from Invitrogen). The clone was sequenced for verification. A further recombination was performed to introduce the ORF into pDEST17 to be expressed by the T7 promoter, yielding pAX2530. The presence and orientation of the inserted axmi-031 fragment were verified by restriction digest, and transformed into *E. coli* BL21 (DE3) cells. This vector produces a translational fusion of 26 amino acids (3.17 kDa), including a 6xHis tag, on the N-terminus of AXMI-031.

[0116] His-AXMI-031 was expressed from pAX2530 in BL21*(DE3) cells as follows. A starter culture of pAX2530 was grown overnight at 37° C. in LB with 50 µg/ml carbenicillin. The following day the saturated culture was diluted 1:100 into fresh medium, and the fresh culture grown at 37° to an OD of 0.4, at which time the culture was placed at room temperature with shaking overnight. As a control, an expression vector carrying the axmi-004 gene (pAX2530) was constructed as for axmi-031, and the AXMI-004 protein (U.S. patent application Ser. No. 10/782,020) was expressed from pAX2504 in the same *E. coli* host. Whole cultures were analyzed by SDS-PAGE. Cultures containing pAX2530 produced a prominent protein band at approximately 135 kDa, the expected size for His-AXMI-031 protein, while cultures containing pAX2504 did not.

Example 9

Antibodies to AXMI-031

[0117] To generate anti-AXMI-031 antibodies, affinity purified AXMI-031 (SEQ ID NO:2) protein was inoculated into rabbits, and antisera to AXMI-031 isolated and titered as known in the art. The selected antisera were found to also react with SYNAXMI-031 protein (SEQ ID NO:8).

Example 10

Activity of AXMI-031 on *C. elegans*

[0118] Cultures of *E. coli* containing pAX2530, were prepared, and found to produce a 135 kDa protein not present in control strains, suggesting the expression of AXMI-031 in pAX2530 containing strains. These cultures were tested for activity on *C. elegans* and were active against *C. elegans*, while control cultures showed no activity against *C. elegans*.

Example 11

Expression of AXMI-031 in *Bacillus*

[0119] The insecticidal gene axmi-031 is amplified by PCR from pAX980, and the PCR product is cloned into the *Bacillus* expression vector pAX916, or another suitable vector, by methods well known in the art. The resulting *Bacillus* strain, containing the vector with axmi-031 is cultured on a conventional growth media, such as CYS media (10 g/l Bacto-casitone; 3 g/l yeast extract; 6 g/l KH₂PO₄; 14 g/l K₂HPO₄; 0.5 mM MgSO₄; 0.05 mM MnCl₂; 0.05 mM FeSO₄), until sporulation is evident by microscopic examination. Samples are prepared, and AXMI-031 protein was tested for activity in bioassays against *C. elegans*, and found to have activity.

Example 12

synaxmi-031, synaxmi-031(apo) and synaxmi-031 (ER)

[0120] In one aspect of the invention, synthetic axmi-031 sequences are generated, for example synaxmi-031 (SEQ ID NO:7). These synthetic sequences have an altered DNA sequence relative to the axmi-031 sequence, and encode a protein that is collinear with the original AXMI-031 protein, but lacks the C-terminal "crystal domain" present in AXMI-031. The synaxmi-031 gene sequence encodes SYNAXMI-031 protein (SEQ ID NO:8), which comprises the first 685 amino acids of the AXMI-031 protein.

[0121] In another aspect of the invention, modified versions of synaxmi-031 are designed such that the resulting peptide is targeted to a plant organelle, such as the endoplasmic reticulum or the apoplast. Peptide sequences known to result in targeting of fusion proteins to plant organelles are known in the art. For example, the N-terminal region of the acid phosphatase gene from the White Lupin *Lupinus albus* (Genebank ID GI:14276838; Miller et al. (2001) Plant Physiology 127: 594-606) is known in the art to result in endoplasmic reticulum targeting of heterologous proteins. If the resulting fusion protein also contains an endoplasmic retention sequence comprising the peptide N-terminus-lysine-aspartic acid-glutamic acid-leucine (i.e. the "KDEL")

motif (SEQ ID NO:36) at the C-terminus, the fusion protein will be targeted to the endoplasmic reticulum. If the fusion protein lacks an endoplasmic reticulum targeting sequence at the C-terminus, the protein will be targeted to the endoplasmic reticulum, but will ultimately be sequestered in the apoplast.

[0122] Thus, the synaxmi-031ER gene (SEQ ID NO: 11) encodes a fusion protein that contains the N-terminal thirty-one amino acids of the acid phosphatase gene from the White Lupin *Lupinus albus* fused to the N-terminus of SYNAXMI-031, as well as the KDEL sequence at the C-terminus. Thus, the resulting protein AXMI-031ER (SEQ ID NO:12), is predicted to be targeted to the plant endoplasmic reticulum upon expression in a plant cell.

[0123] The synaxmi-031(apo) gene (SEQ ID NO:9) encodes a fusion protein that contains the N-terminal thirty-one amino acids of the acid phosphatase gene from the White Lupin *Lupinus albus* fused to the N-terminus of SYNAXMI-031, but lacks the KDEL sequence at the C-terminus. Thus, the resulting protein AXMI-031 (APO) (SEQ ID NO:10), is predicted to be targeted to the plant apoplast upon expression in a plant cell.

Example 13

Truncations of synaxmi-031 to Yield Alternate AXMI-031 Proteins

[0124] DNA constructs that resulted in expression of variants of AXMI-031 protein were developed and expressed, in addition to synthetic sequences encoding AXMI-031 and variants and fragments thereof (SEQ ID NO: 15-27). A subset of these genes were tested for nematode activity in vitro.

TABLE 4

Nematicidal Activity of AXMI-031 variants in vitro			
Protein	Nucleotide SEQ ID NO:	Amino acid SEQ ID NO:	Active on <i>C. elegans</i> ?
Bacterial Expression			
AXMI-031-truncated	14	15	Yes
AXMI-031(ml)	16	17	Yes
AXMI-031(ml)-truncated	18	19	Yes
AXMI-031(A-D)	20	21	Yes
SYNAXMI-031 (A-D)	26	27	NT
AXMI-031(B-C)	22	23	Yes
AXMI-031(B-D)	24	25	Yes

NT = not tested

Example 14

Truncations and Addition of Cellular Targeting Domain(s) for Plant Expression

[0125] In another aspect of the invention, modified versions of the synaxmi-031 sequences are designed such that the resulting peptide is targeted to a plant organelle, such as the endoplasmic reticulum or the apoplast.

[0126] In another aspect of the invention, the genes are truncated such that the resulting peptide is a truncated

version of AXMI-031, which may or may not be further modified for targeting to plant organelles, such as the apoplast or the endoplasmic reticulum.

[0127] In another aspect of the invention, modified versions are developed that result in expression of truncated variants that contain domains designed to target the resulting protein to plant organelles.

[0128] The following variant nucleotide sequences were designed:

[0129] aposynaxmi-031 (A-D) (SEQ ID NO:28) encodes the APOAXMI-031 (A-D) protein (SEQ ID NO:29). apoSyn2axmi-031(A-D) (SEQ ID NO:30) encodes the APOAXMI-031(A-D) protein (SEQ ID NO:31). aposynaxmi-031J1) (SEQ ID NO:37) encodes the APOSYNAXMI-031(FL) protein (SEQ ID NO:38). Synaxmi031(fl)-ER (SEQ ID NO:32) encodes the SYNAXMI-031(FL)-ER protein (SEQ ID NO:33).

Example 15

Extraction of Plasmid DNA from Strains ATX16538 ATX16093 and ATX21049

[0130] Strains ATX16538, ATX16093, and ATX21049 were selected for analysis. Pure cultures of each strain were grown in large quantities of rich media. The cultures were centrifuged to harvest the cell pellet. The cell pellet was then prepared by treatment with SDS by methods known in the art, resulting in breakage of the cell wall and release of DNA. Proteins and large genomic DNA was then precipitated by a high salt concentration. The plasmid DNA was then precipitated with ethanol. In several instances, the plasmid DNA was separated from any remaining chromosomal DNA by high-speed centrifugation through a cesium chloride gradient. Alternatively, the plasmid DNA was purified by binding to a resin, as known in the art. For each strain, the quality of the DNA was checked by visualization on an agarose gel by methods known in the art.

Example 16

Cloning of Genes from Strains ATX16538 ATX16093 and ATX21049

[0131] DNA libraries were prepared from the plasmid DNA of each strain. This may be achieved in many ways as known in the art. For, example, the purified plasmid DNA can be sheared into 5-10 kb sized fragments and the 5' and 3' single stranded overhangs repaired using T4 DNA polymerase and Klenow fragment in the presence of all four dNTPs, as known in the art. Phosphates can then be attached to the 5' ends by treatment with T4 polynucleotide kinase, as known in the art. The repaired DNA fragments can then be ligated overnight into a standard high copy vector (i.e. pBLUESCRIPT® SK+), suitably prepared to accept the inserts as known in the art (for example by digestion with a restriction enzyme producing blunt ends).

[0132] The quality of the resulting DNA libraries was analyzed by digesting a subset of clones with a restriction enzyme known to have a cleavage site flanking the cloning site. A high percentage of clones were determined to contain inserts, usually with an average insert size of 5-6 kb.

Example 17

High Throughput Sequencing of Library Plates

[0133] Once the DNA library quality was checked and confirmed, colonies were grown in a rich broth in 2 ml 96-well blocks overnight at 37° C., typically at a shaking speed of 350 rpm. The blocks were centrifuged to collect the cells at the bottom of the block. The blocks were then prepared by standard alkaline lysis prep in a high throughput format.

[0134] The end sequences of clones from this library were then determined for a large number of clones from each block in the following manner: The DNA sequence of each clone chosen for analysis was determined using the fluorescent dye terminator sequencing technique (Applied Biosystems), by methods known in the art using an automated DNA sequencing machine, and standard oligonucleotide primers that anneal to the plasmid vector in the region flanking the insert.

Example 18

Assembly and Screening of Sequencing Data

[0135] DNA sequences obtained were compiled into an assembly project and aligned together to form contigs. This can be done efficiently using a computer program, such as Vector NTi, or alternatively by using the Pred/Phrap suite of DNA alignment and analysis programs as described elsewhere herein. These contigs, along with any individual read that may not have been added to a contig, were compared to a compiled database of all classes of known pesticidal genes. Contigs or individual reads identified as having identity to a known endotoxin or pesticidal gene were analyzed further.

[0136] From strain ATX16538, pAX2579 was found to contain an open reading frame with homology to “cry” type delta-endotoxins. This open reading frame was designated as axmi-039 (SEQ ID NO:3), and the encoded protein was designated AXMI-039 (SEQ ID NO:5). The axmi-039 ORF and flanking sequence (151 bp upstream of the start codon and 29 bp downstream of the stop codon) was PCR amplified, cloned into pRSFIB and sequenced to yield pAX2579. pAX2579 was deposited with the ARS Patent Strain Collection on Jun. 9, 2006, and assigned NRRL B-30936. AXMI-039 is 43.9% amino acid sequence identity to Cry5Ba1, which is the closest homolog identified.

[0137] From strain ATX16093, pAX4313 was found to contain an open reading frame with homology to “cry” type delta-endotoxins. This open reading frame was designated as axmi-040 (SEQ ID NO:7), and the encoded protein was designated AXMI-040 (SEQ ID NO:8). pAX4313 was deposited with the ARS Patent Strain Collection on Jun. 9, 2006, and assigned NRRL B-30937. AXMI-040 is 42.9% amino acid sequence identity to Cry21Ba1, which is the closest homolog identified.

[0138] From strain ATX21049, an open reading frame was identified that exhibited homology to “cry” type delta-endotoxins. This open reading frame was designated as axmi-049 (SEQ ID NO:34), and the encoded protein was designated AXMI-049 (SEQ ID NO:35). This open reading frame was amplified by PCR and cloned into a vector to yield pAX5039. pAX5039 was deposited with the ARS

Patent Strain Collection on May 29, 2007, and assigned NRRL B-50046. AXMI-049 has 46.1% amino acid sequence identity to Cry21Ba1, which is the closest homology identified.

Example 19

Vectoring of the Pesticidal Genes of the Invention for Plant Expression

[0139] Each of the coding regions of the genes of the invention are connected independently with appropriate promoter and terminator sequences for expression in plants. Such sequences are well known in the art and may include the rice actin promoter or maize ubiquitin promoter for expression in monocots, the Arabidopsis UBQ3 promoter or CaMV 35S promoter for expression in dicots, and the nos or PinII terminators. Techniques for producing and confirming promoter—gene—terminator constructs also are well known in the art.

Example 20

Transformation of the Genes of the Invention into Plant Cells by Agrobacterium-Mediated Transformation

[0140] Ears are collected 8-12 days after pollination. Embryos are isolated from the ears, and those embryos 0.8-1.5 mm in size are used for transformation. Embryos are plated scutellum side-up on a suitable incubation media, and incubated overnight at 25° C. in the dark. However, it is not necessary per se to incubate the embryos overnight. Embryos are contacted with an *Agrobacterium* strain containing the appropriate vectors for Ti plasmid mediated transfer for 5-10 min, and then plated onto co-cultivation media for 3 days (25° C. in the dark). After co-cultivation, explants are transferred to recovery period media for five days (at 25° C. in the dark). Explants are incubated in selection media for up to eight weeks, depending on the nature and characteristics of the particular selection utilized. After the selection period, the resulting callus is transferred to embryo maturation media, until the formation of mature somatic embryos is observed. The resulting mature somatic embryos are then placed under low light, and the process of regeneration is initiated as known in the art. The resulting shoots are allowed to root on rooting media, and the resulting plants are transferred to nursery pots and propagated as transgenic plants.

Example 21

Transgenic Plants Expressing AXMI-031 and Variants

[0141] The plant expression cassettes described herein are combined with an appropriate plant selectable marker to aid in the selections of transformed cells and tissues, and ligated into plant transformation vectors. These may include binary vectors from *Agrobacterium*-mediated transformation or simple plasmid vectors for aerosol or biolistic transformation. synaxmi-031 (apo) was cloned into a plant expression vector, and this vector was introduced into *Agrobacterium tumefaciens* as known in the art. The synaxmi-031 (apo) coding region under control of the Arabidopsis UBQ3 promoter (Norris et al. (1993) *J. Plant Mol. Biol.* 21:895-

906) was introduced into *Arabidopsis thaliana* by floral dip method as known in the art, and transgenic plants were selected. The presence of synaxmi-031(apo) in the transgenic Ti population was confirmed by PCR analysis as known in the art, using oligonucleotide primers derived from the sequence of synaxmi-031, which also anneal to synaxmi-031 (apo).

[0142] Leaf and root tissue from transgenic synaxmi-031 (apo) containing plants was prepared and separated on polyacrylamide gels alongside non-transgenic controls and dilutions of AXMI-031 protein, and transferred to a membrane as known in the art. The samples were tested for the presence of the expression product of synaxmi-031(apo) by Western blot analysis as known in the art, using anti-AXMI-031 antibodies described herein. The expression product of synaxmi-031 (apo) of the expected size was detected in samples of both leaf and root tissue from transgenic synaxmi-031(apo)-containing plants, but not detected in non-transgenic controls.

TABLE 5

Antibody detection of SYNAXMI-031(APO) in transgenic plants	
Source of Tissue	Detection of SYNAXMI-031(APO)
Non-transformed control	—
synaxmi-031 (apo)	+++
containing plant 'A'	
synaxmi-031(apo)	+++
containing plant 'B'	

Example 22

Reduced Cyst Formation by AXMI-031 Expressing Plants

[0143] Transgenic plants expressing synaxmi-031 (apo) were tested for ability to resist infestation by *Heterodera schachtii* compared to control plants. Transgenic plants, as well as control plants transformed with vector alone, were infested with approximately 100 J2 hatchlings, and the number of nematodes entering the roots, as well as the number of cyst formed, was measured. Transgenic plants expressing SYNAXMI-031 (APO) were found to consistently have reduced numbers of nematodes entering the roots, and reduced numbers of cysts formed relative to controls.

TABLE 6

Reduced cyst formation in AXMI-031 expressing plants	
	Cyst formation
Control plant	++
Plants expressing AXMI-031(APO)	+

Example 23

Additional Assays for Pesticidal Activity

[0144] The ability of a pesticidal protein to act as a pesticide upon a pest is often assessed in a number of ways.

One way well known in the art is to perform a feeding assay. In such a feeding assay, one exposes the pest to a sample containing either compounds to be tested, or control samples. Often this is performed by placing the material to be tested, or a suitable dilution of such material, onto a material that the pest will ingest, such as an artificial diet. The material to be tested may be composed of a liquid, solid, or slurry. The material to be tested may be placed upon the surface and then allowed to dry. Alternatively, the material to be tested may be mixed with a molten artificial diet, then dispensed into the assay chamber. The assay chamber may be, for example, a cup, a dish, or a well of a microtiter plate.

[0145] Assays for sucking pests (for example aphids) may involve separating the test material from the insect by a partition, ideally a portion that can be pierced by the sucking mouth parts of the sucking insect, to allow ingestion of the test material. Often the test material is mixed with a feeding stimulant, such as sucrose, to promote ingestion of the test compound.

[0146] Other types of assays can include microinjection of the test material into the mouth, or gut of the pest, as well as development of transgenic plants, followed by test of the ability of the pest to feed upon the transgenic plant. Plant testing may involve isolation of the plant parts normally consumed, for example, small cages attached to a leaf, or isolation of entire plants in cages containing insects.

[0147] Other methods and approaches to assay pests are known in the art, and can be found, for example in Robertson, J. L. & H. K. Preisler. 1992. *Pesticide bioassays with arthropods*. CRC, Boca Raton, FL. Alternatively, assays are commonly described in the journals "Arthropod Management Tests" and "Journal of Economic Entomology" or by discussion with members of the Entomological Society of America (ESA).

Example 24

Transformation of Maize Cells with the Pesticidal Genes of the Invention

[0148] Maize ears are collected 8-12 days after pollination. Embryos are isolated from the ears, and those embryos 0.8-1.5 mm in size are used for transformation. Embryos are plated scutellum side-up on a suitable incubation media, such as DN62A5S media (3.98 g/L N6 Salts; 1 mL/L (of 1000xStock) N6 Vitamins; 800 mg/L L-Asparagine; 100 mg/L Myo-inositol; 1.4 g/L L-Proline; 100 mg/L Casaminoacids; 50 g/L sucrose; 1 mL/L (of 1 mg/mL Stock) 2,4-D), and incubated overnight at 25° C. in the dark.

[0149] The resulting explants are transferred to mesh squares (30-40 per plate), transferred onto osmotic media for 30-45 minutes, then transferred to a beaming plate (see, for example, PCT Publication No. WO/0138514 and U.S. Pat. No. 5,240,842).

[0150] DNA constructs designed to express the genes of the invention in plant cells are accelerated into plant tissue using an aerosol beam accelerator, using conditions essentially as described in PCT Publication No. WO/01385 14. After beaming, embryos are incubated for 30 min on osmotic media, then placed onto incubation media overnight

at 25° C. in the dark. To avoid unduly damaging beamed explants, they are incubated for at least 24 hours prior to transfer to recovery media. Embryos are then spread onto recovery period media, for 5 days, 25° C. in the dark, then transferred to a selection media. Explants are incubated in selection media for up to eight weeks, depending on the nature and characteristics of the particular selection utilized. After the selection period, the resulting callus is transferred to embryo maturation media, until the formation of mature somatic embryos is observed. The resulting mature somatic embryos are then placed under low light, and the process of regeneration is initiated by methods known in the art. The resulting shoots are allowed to root on rooting media, and the resulting plants are transferred to nursery pots and propagated as transgenic plants.

DN62A5S Media		
Components	per liter	Source
Chu's N6 Basal Salt Mixture (Prod. No. C 416)	3.98 g/L	Phytotechnology Labs
Chu's N6 Vitamin Solution (Prod. No. C 149)	1 mL/L (of 1000 × Stock)	Phytotechnology Labs
L-Asparagine	800 mg/L	Phytotechnology Labs
Myo-inositol	100 mg/L	Sigma
L-Proline	1.4 g/L	Phytotechnology Labs
Casaminoacids	100 mg/L	Fisher Scientific

-continued

DN62A5S Media		
Components	per liter	Source
Sucrose	50 g/L	Phytotechnology Labs
2,4-D (Prod. No. D-7299)	1 mL/L (of 1 mg/mL Stock)	Sigma

[0151] Adjust the pH of the solution to pH to 5.8 with 1N KOH/1N KCl, add Gelrite (Sigma) to 3g/L, and autoclave. After cooling to 50° C., add 2 ml/L of a 5 mg/ml stock solution of Silver Nitrate (Phytotechnology Labs). Recipe yields about 20 plates.

[0152] All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

[0153] Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

SEQUENCE LISTING

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<210> SEQ ID NO 1

<211> LENGTH: 3558

<212> TYPE: DNA

<213> ORGANISM: *Bacillus cereus/Bacillus thuringiensis*

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)...(3558)

<400> SEQUENCE: 1

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1          5          10          15

gca ata cca gta tct aat gtt aat tcg ttg act gat aca gtt gga gat      96
Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp
20          25          30

tta aaa aaa gca tgg gaa gaa ttt caa aaa act ggt tct ttt tca tta      144
Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu
35          40          45

aca gct tta caa caa gga ttt tct gct tca caa gga gga aca ttc aat      192
Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn
50          55          60

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65          70          75          80

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Thr	Tyr	Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	Ile		
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Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Phe		
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Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser		
355								360				365					
tat	tat	aat	gat	gaa	tta	caa	aat	cta	gaa	tta	gga	gta	tat	acc	cct	1152	
Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	Pro		
370								375				380					
cct	aaa	aaa	gga	agt	gga	tac	tct	tat	cct	tat	gga	ttt	gtt	tta	aat	1200	
Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn		

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385	390	395	400	
tat gca aac agt aaa tat aaa tat ggt gat agc aat gat cca gaa tct				1248
Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser				
	405	410	415	
cta gga gga tta tct aca cta tct gca cct ata caa caa gtt aat gca				1296
Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala				
	420	425	430	
gca act caa aac agt aaa tat cta gat gga gaa atc cta aat gga ata				1344
Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile				
	435	440	445	
gga gca tcc tta cct ggt tat tgt act aca gga tgt tca cca aca gaa				1392
Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu				
	450	455	460	
cca cct ttt agt tgt act tct acc gct aat ggc tat aaa gca agc tgt				1440
Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys				
	465	470	475	480
aat cct tca gat aca aat caa aaa att aac gct tta tat cct ttt aca				1488
Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr				
	485	490	495	
caa gct aat gta aag gga aac aca gga aaa tta gga gta ctg gca agt				1536
Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser				
	500	505	510	
ctt gtt tca tat gat tta aat cct aaa aat gta ttt ggt gaa tta gat				1584
Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp				
	515	520	525	
tca gat aca aat aat gtt atc tta aaa gga att cct gca gaa aaa gga				1632
Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly				
	530	535	540	
tat ttt cct aat aat gcg cgt cct act gtt gta aaa gaa tgg att aat				1680
Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn				
	545	550	555	560
ggt gca agt gct gta cca ctt gat tca gga aat acc tta ttt atg acg				1728
Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr				
	565	570	575	
gct acg aat tta aca gct act caa tat aga att aga ata cgt tat gca				1776
Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala				
	580	585	590	
aat cca aat tca aat act caa atc ggt gta cga att aca caa aat ggt				1824
Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly				
	595	600	605	
tct cta att tcc agt agt aat cta aca ctt tat agt act act gat atg				1872
Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met				
	610	615	620	
aat aat act tta cca cta aat gta tat gta ata gga gaa aat gga aat				1920
Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn				
	625	630	635	640
tat aca ctt caa gat tta tat aat act act aat gtt tta tca aca gga				1968
Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly				
	645	650	655	
gat att aca tta caa att aca gga gga gat caa aaa ata ttt att gat				2016
Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp				
	660	665	670	
cga ata gaa ttt gtt cct act atg cct gta cct ggt aat act aac aac				2064
Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn Asn				
	675	680	685	
aat aac ggt aat aat aac ggt aat aat aat ccc cca cac cac gtt tgt				2112
Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val Cys				

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690	695	700	
gca ata gct ggt aca caa caa tct tgt tct gga ccg ccc aaa ttt gaa Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe Glu 705 710 715 720			2160
caa gta agt gat tta gaa aaa att aca aca caa gta tat atg tta ttc Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu Phe 725 730 735			2208
aaa tct tct ccg tat gaa gaa tta gct cta gaa gtt tcc agc tat caa Lys Ser Ser Pro Tyr Glu Glu Leu Ala Leu Glu Val Ser Ser Tyr Gln 740 745 750			2256
att agt caa gta gca tta aaa gtt atg gca tta tct gat gaa cta ttt Ile Ser Gln Val Ala Leu Lys Val Met Ala Leu Ser Asp Glu Leu Phe 755 760 765			2304
tgt gaa gaa aaa aac gta tta cga aaa tta gtc aat aaa gca aaa caa Cys Glu Glu Lys Asn Val Leu Arg Lys Leu Val Asn Lys Ala Lys Gln 770 775 780			2352
tta tta gaa gca agt aac tta cta gta ggt gga aat ttt gaa aca act Leu Leu Glu Ala Ser Asn Leu Leu Val Gly Gly Asn Phe Glu Thr Thr 785 790 795 800			2400
caa aat tgg gta ctt gga aca aat gct tat ata aat tat gat tcg ttt Gln Asn Trp Val Leu Gly Thr Asn Ala Tyr Ile Asn Tyr Asp Ser Phe 805 810 815			2448
tta ttt aat gga aat tat tta tct tta caa cca gca agt gga ttt ttc Leu Phe Asn Gly Asn Tyr Leu Ser Leu Gln Pro Ala Ser Gly Phe Phe 820 825 830			2496
aca tct tat gct tat caa aaa ata gat gag tca aca tta aaa cca tat Thr Ser Tyr Ala Tyr Gln Lys Ile Asp Glu Ser Thr Leu Lys Pro Tyr 835 840 845			2544
aca cga tat aaa gtt tct ggg ttc att ggg caa agt aat caa gta gaa Thr Arg Tyr Lys Val Ser Gly Phe Ile Gly Gln Ser Asn Gln Val Glu 850 855 860			2592
ctt att att tct cgt tat gga aaa gaa att gat aaa ata tta aat gtt Leu Ile Ile Ser Arg Tyr Gly Lys Glu Ile Asp Lys Ile Leu Asn Val 865 870 875 880			2640
cca tat gca gga cct ctt cct atc act gct gat gca tca ata act tgt Pro Tyr Ala Gly Pro Leu Pro Ile Thr Ala Asp Ala Ser Ile Thr Cys 885 890 895			2688
tgt gca cca gaa ata ggc caa tgt gat ggg gaa caa tct gat tct cat Cys Ala Pro Glu Ile Gly Gln Cys Asp Gly Glu Gln Ser Asp Ser His 900 905 910			2736
ttc ttt aac tat agc atc gat gta ggt gca ctt cac cca gaa tta aac Phe Phe Asn Tyr Ser Ile Asp Val Gly Ala Leu His Pro Glu Leu Asn 915 920 925			2784
cct ggc att gaa att ggt ctt aaa att gtg caa tca aat ggt tat ata Pro Gly Ile Glu Ile Gly Leu Lys Ile Val Gln Ser Asn Gly Tyr Ile 930 935 940			2832
aca att agt aat cta gaa att att gaa gaa cgt cca ctt aca gaa atg Thr Ile Ser Asn Leu Glu Ile Ile Glu Glu Arg Pro Leu Thr Glu Met 945 950 955 960			2880
gaa att caa gca gtc aat cga aaa aat caa aaa tgg gaa aga gaa aaa Glu Ile Gln Ala Val Asn Arg Lys Asn Gln Lys Trp Glu Arg Glu Lys 965 970 975			2928
ctt cta gaa tgt gca agt att agt gaa ctt tta caa cca att att aat Leu Leu Glu Cys Ala Ser Ile Ser Glu Leu Leu Gln Pro Ile Ile Asn 980 985 990			2976
caa atc gat tca ttg ttt aaa gat gga aac tgg tat aat gat att ctt Gln Ile Asp Ser Leu Phe Lys Asp Gly Asn Trp Tyr Asn Asp Ile Leu			3024

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995	1000	1005	
cct cat gtc aca tat	caa gat tta aaa aat att	ata ata ccc gag tta	3072
Pro His Val Thr Tyr	Gln Asp Leu Lys Asn Ile	Ile Ile Pro Glu Leu	
1010	1015	1020	
cca aaa tta aaa cat	tggttc ata gag aat ctc	cca ggt gaa tat cat	3120
Pro Lys Leu Lys His	Trp Phe Ile Glu Asn	Leu Pro Gly Glu Tyr His	
1025	1030	1035 1040	
gaa att gaa caa aaa atg	aaa gaa gct cta aaa tat	gca ttt aca caa	3168
Glu Ile Glu Gln Lys	Met Lys Glu Ala Leu	Lys Tyr Ala Phe Thr Gln	
1045	1050	1055	
tta gac gag aaa aat tta atc	cac aat ggt cac ttt aca act	aac tta	3216
Leu Asp Glu Lys Asn	Leu Ile His Asn Gly	His Phe Thr Thr Asn Leu	
1060	1065	1070	
ata gat tgg caa gta gaa ggt	gat gct caa atg aaa gta tta	gaa aat	3264
Ile Asp Trp Gln Val	Glu Gly Asp Ala Gln Met	Lys Val Leu Glu Asn	
1075	1080	1085	
gat gct ctt gca tta caa ctt	ttc aac tgg gat gct agt	gct tca caa	3312
Asp Ala Leu Ala Leu	Gln Leu Phe Asn Trp	Asp Ala Ser Ala Ser Gln	
1090	1095	1100	
tct ata aat ata tta gaa ttt	gat gaa gat aag gca tat	aaa ctt cgc	3360
Ser Ile Asn Ile Leu	Glu Phe Asp Glu Asp	Lys Ala Tyr Lys Leu Arg	
1105	1110	1115 1120	
gta tat gct caa gga agc gga	aca atc caa ttt gga aac	tgt gaa gat	3408
Val Tyr Ala Gln Gly	Ser Gly Thr Ile Gln	Phe Gly Asn Cys Glu Asp	
1125	1130	1135	
gaa gct atc caa ttt aat aca	aac tca ttc ata tat caa	gaa aaa ata	3456
Glu Ala Ile Gln Phe	Asn Thr Asn Ser Phe	Ile Tyr Gln Glu Lys Ile	
1140	1145	1150	
gtc tat ttc gat acc cca tca	gtt aat tta cac ata caa	tca gaa ggt	3504
Val Tyr Phe Asp Thr	Pro Ser Val Asn Leu	His Ile Gln Ser Glu Gly	
1155	1160	1165	
tct gaa ttt att gta agt agt	atc gat cta att gaa tta	tca gac gac	3552
Ser Glu Phe Ile Val	Ser Ile Asp Leu Ile	Glu Leu Ser Asp Asp	
1170	1175	1180	
caa taa			3558
Gln *			
1185			

<210> SEQ ID NO 2

<211> LENGTH: 1185

<212> TYPE: PRT

<213> ORGANISM: Bacillus cereus/Bacillus thuringiensis

<400> SEQUENCE: 2

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Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp
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Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu
35 40 45

Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn
50 55 60

Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val
65 70 75 80

Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp
85 90 95

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Leu	Trp	Pro	His	Lys	Asn	Lys	Asn	Ala	Asp	Thr	Glu	Asn	Leu	Ile	Asn
			100					105					110		
Leu	Ile	Asp	Ser	Glu	Ile	Gln	Lys	Gln	Leu	Asn	Lys	Ala	Leu	Leu	Asp
		115					120					125			
Ala	Asp	Arg	Asn	Glu	Trp	Ser	Ser	Tyr	Leu	Glu	Ser	Ile	Phe	Asp	Ser
		130				135					140				
Ser	Asn	Asn	Leu	Asn	Gly	Ala	Ile	Val	Asp	Ala	Gln	Trp	Ser	Gly	Thr
145					150				155					160	
Val	Asn	Thr	Thr	Asn	Arg	Thr	Leu	Arg	Asn	Pro	Thr	Glu	Ser	Asp	Tyr
				165					170					175	
Thr	Asn	Val	Val	Thr	Asn	Phe	Ile	Ala	Ala	Asp	Gly	Asp	Ile	Ala	Asn
			180					185					190		
Asn	Glu	Asn	His	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala	Ala	Ala	Pro
		195					200					205			
Tyr	Phe	Val	Ile	Gly	Ala	Thr	Ala	Arg	Phe	Ala	Ala	Met	Gln	Ser	Tyr
	210					215				220					
Ile	Lys	Phe	Cys	Asn	Ala	Trp	Ile	Asp	Lys	Val	Gly	Leu	Ser	Asp	Ala
225					230				235					240	
Gln	Leu	Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys	Gln	Asn	Met
				245					250					255	
Arg	Asn	Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys	Val	Phe	Lys
			260					265					270		
Asp	Ser	Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val	Asp
		275					280					285			
Thr	Tyr	Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	Ile
	290					295					300				
Val	Ala	Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr	Ser	Gln	Thr
305					310				315					320	
Ala	Leu	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	Glu
				325					330					335	
Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Phe
			340					345					350		
Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser
		355				360						365			
Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	Pro
	370					375					380				
Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn
385					390				395					400	
Tyr	Ala	Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu	Ser
				405					410					415	
Leu	Gly	Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn	Ala
			420					425					430		
Ala	Thr	Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu	Asn	Gly	Ile
			435				440					445			
Gly	Ala	Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr	Glu
	450					455					460				
Pro	Pro	Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser	Cys
465					470					475				480	
Asn	Pro	Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe	Thr
				485					490					495	
Gln	Ala	Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	Ser

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500						505						510					
Leu	Val	Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu	Asp		
		515					520					525					
Ser	Asp	Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys	Gly		
	530					535					540						
Tyr	Phe	Pro	Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu	Trp	Ile	Asn		
545					550					555					560		
Gly	Ala	Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met	Thr		
				565					570					575			
Ala	Thr	Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr	Ala		
			580					585						590			
Asn	Pro	Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn	Gly		
		595					600					605					
Ser	Leu	Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp	Met		
	610					615					620						
Asn	Asn	Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly	Asn		
625					630					635					640		
Tyr	Thr	Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr	Gly		
				645					650					655			
Asp	Ile	Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile	Asp		
			660					665					670				
Arg	Ile	Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn	Thr	Asn	Asn		
	675						680					685					
Asn	Asn	Gly	Asn	Asn	Asn	Gly	Asn	Asn	Asn	Pro	Pro	His	His	Val	Cys		
	690					695					700						
Ala	Ile	Ala	Gly	Thr	Gln	Gln	Ser	Cys	Ser	Gly	Pro	Pro	Lys	Phe	Glu		
705					710					715					720		
Gln	Val	Ser	Asp	Leu	Glu	Lys	Ile	Thr	Thr	Gln	Val	Tyr	Met	Leu	Phe		
				725					730					735			
Lys	Ser	Ser	Pro	Tyr	Glu	Glu	Leu	Ala	Leu	Glu	Val	Ser	Ser	Tyr	Gln		
			740					745					750				
Ile	Ser	Gln	Val	Ala	Leu	Lys	Val	Met	Ala	Leu	Ser	Asp	Glu	Leu	Phe		
	755						760					765					
Cys	Glu	Glu	Lys	Asn	Val	Leu	Arg	Lys	Leu	Val	Asn	Lys	Ala	Lys	Gln		
	770					775					780						
Leu	Leu	Glu	Ala	Ser	Asn	Leu	Leu	Val	Gly	Gly	Asn	Phe	Glu	Thr	Thr		
785					790					795					800		
Gln	Asn	Trp	Val	Leu	Gly	Thr	Asn	Ala	Tyr	Ile	Asn	Tyr	Asp	Ser	Phe		
				805					810					815			
Leu	Phe	Asn	Gly	Asn	Tyr	Leu	Ser	Leu	Gln	Pro	Ala	Ser	Gly	Phe	Phe		
			820					825					830				
Thr	Ser	Tyr	Ala	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Thr	Leu	Lys	Pro	Tyr		
	835						840					845					
Thr	Arg	Tyr	Lys	Val	Ser	Gly	Phe	Ile	Gly	Gln	Ser	Asn	Gln	Val	Glu		
	850					855					860						
Leu	Ile	Ile	Ser	Arg	Tyr	Gly	Lys	Glu	Ile	Asp	Lys	Ile	Leu	Asn	Val		
865					870					875					880		
Pro	Tyr	Ala	Gly	Pro	Leu	Pro	Ile	Thr	Ala	Asp	Ala	Ser	Ile	Thr	Cys		
				885					890					895			
Cys	Ala	Pro	Glu	Ile	Gly	Gln	Cys	Asp	Gly	Glu	Gln	Ser	Asp	Ser	His		
			900					905					910				

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Phe Phe Asn Tyr Ser Ile Asp Val Gly Ala Leu His Pro Glu Leu Asn
 915 920 925
 Pro Gly Ile Glu Ile Gly Leu Lys Ile Val Gln Ser Asn Gly Tyr Ile
 930 935 940
 Thr Ile Ser Asn Leu Glu Ile Ile Glu Glu Arg Pro Leu Thr Glu Met
 945 950 955 960
 Glu Ile Gln Ala Val Asn Arg Lys Asn Gln Lys Trp Glu Arg Glu Lys
 965 970 975
 Leu Leu Glu Cys Ala Ser Ile Ser Glu Leu Leu Gln Pro Ile Ile Asn
 980 985 990
 Gln Ile Asp Ser Leu Phe Lys Asp Gly Asn Trp Tyr Asn Asp Ile Leu
 995 1000 1005
 Pro His Val Thr Tyr Gln Asp Leu Lys Asn Ile Ile Ile Pro Glu Leu
 1010 1015 1020
 Pro Lys Leu Lys His Trp Phe Ile Glu Asn Leu Pro Gly Glu Tyr His
 1025 1030 1035 1040
 Glu Ile Glu Gln Lys Met Lys Glu Ala Leu Lys Tyr Ala Phe Thr Gln
 1045 1050 1055
 Leu Asp Glu Lys Asn Leu Ile His Asn Gly His Phe Thr Thr Asn Leu
 1060 1065 1070
 Ile Asp Trp Gln Val Glu Gly Asp Ala Gln Met Lys Val Leu Glu Asn
 1075 1080 1085
 Asp Ala Leu Ala Leu Gln Leu Phe Asn Trp Asp Ala Ser Ala Ser Gln
 1090 1095 1100
 Ser Ile Asn Ile Leu Glu Phe Asp Glu Asp Lys Ala Tyr Lys Leu Arg
 1105 1110 1115 1120
 Val Tyr Ala Gln Gly Ser Gly Thr Ile Gln Phe Gly Asn Cys Glu Asp
 1125 1130 1135
 Glu Ala Ile Gln Phe Asn Thr Asn Ser Phe Ile Tyr Gln Glu Lys Ile
 1140 1145 1150
 Val Tyr Phe Asp Thr Pro Ser Val Asn Leu His Ile Gln Ser Glu Gly
 1155 1160 1165
 Ser Glu Phe Ile Val Ser Ser Ile Asp Leu Ile Glu Leu Ser Asp Asp
 1170 1175 1180
 Gln
 1185

<210> SEQ ID NO 3
 <211> LENGTH: 3984
 <212> TYPE: DNA
 <213> ORGANISM: Unknown
 <220> FEATURE:
 <223> OTHER INFORMATION: Isolated from soil sample
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(3984)

<400> SEQUENCE: 3

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1 5 10 15	
cta ccc att atc ccc aat tct atc tta act ttt gaa gat aat cga aaa	96
Leu Pro Ile Ile Pro Asn Ser Ile Leu Thr Phe Glu Asp Asn Arg Lys	
20 25 30	

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aaa ata gaa gag ggt att aaa gag ttt gaa aag act gga cgt ata aaa Lys Ile Glu Glu Gly Ile Lys Glu Phe Glu Lys Thr Gly Arg Ile Lys 35 40 45	144
ccc ctt aaa gat tta ata gag ctc ata ttc aaa ggg tat agt gac gat Pro Leu Lys Asp Leu Ile Glu Leu Ile Phe Lys Gly Tyr Ser Asp Asp 50 55 60	192
gaa tct tct tac gca gca tta gtt caa act atg ctt gtc gtt att ccc Glu Ser Ser Tyr Ala Ala Leu Val Gln Thr Met Leu Val Val Ile Pro 65 70 75 80	240
ttg gcg ttc cct gaa tta gcc cca gtt ctt cca att att ggc gta gta Leu Ala Phe Pro Glu Leu Ala Pro Val Leu Pro Ile Ile Gly Val Val 85 90 95	288
att aat ttc gtt ttt cca ggt ttg aag ggt tct gct aaa tca acc tat Ile Asn Phe Val Phe Pro Gly Leu Lys Gly Ser Ala Lys Ser Thr Tyr 100 105 110	336
aca atg att aca gag atg gtt gat aaa gcc att aac caa tca ttc acg Thr Met Ile Thr Glu Met Val Asp Lys Ala Ile Asn Gln Ser Phe Thr 115 120 125	384
gcc cag att aca aat ata tta aca aac aat att act ggt ata caa aat Ala Gln Ile Thr Asn Ile Leu Thr Asn Asn Ile Thr Gly Ile Gln Asn 130 135 140	432
aat ata caa tct gtt tac gac gca atg agc aat gcc att gga aca aat Asn Ile Gln Ser Val Tyr Asp Ala Met Ser Asn Ala Ile Gly Thr Asn 145 150 155 160	480
gac aca att cat aat ttc atc aga aat aat gat aca aca cct tgc tct Asp Thr Ile His Asn Phe Ile Arg Asn Asn Asp Thr Thr Pro Cys Ser 165 170 175	528
caa aac aat cag cca gct tgt cct tgt cct cca aat aat caa tgt tta Gln Asn Asn Gln Pro Ala Cys Pro Cys Pro Pro Asn Asn Gln Cys Leu 180 185 190	576
caa aaa gtt gtt gat gaa tat act aaa gca ata gct aat atc gat ctc Gln Lys Val Val Asp Glu Tyr Thr Lys Ala Ile Ala Asn Ile Asp Leu 195 200 205	624
att atc cct caa ttt cat gat cca ctt act ggt gta att tcc gat tta Ile Ile Pro Gln Phe His Asp Pro Leu Thr Gly Val Ile Ser Asp Leu 210 215 220	672
gct act gca aac atg tat att tta cct tta tac gct caa act gtt aat Ala Thr Ala Asn Met Tyr Ile Leu Pro Leu Tyr Ala Gln Thr Val Asn 225 230 235 240	720
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aaa tat gat gaa aaa gaa act gtt ttt cag gct ttt att aat gct gat Lys Tyr Asp Glu Lys Glu Thr Val Phe Gln Ala Phe Ile Asn Ala Asp 260 265 270	816
att cca gaa caa att aaa aaa ctt cgt caa gat att atc acg tat aca Ile Pro Glu Gln Ile Lys Lys Leu Arg Gln Asp Ile Ile Thr Tyr Thr 275 280 285	864
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aat tca aaa aaa caa cta aat gac tat atc cgt tat aca aga att atc Asn Ser Lys Lys Gln Leu Asn Asp Tyr Ile Arg Tyr Thr Arg Ile Ile 305 310 315 320	960
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gtg aat tat gca tta cct gtc caa caa aat atg aca cgc att ata ttt	1056
Val Asn Tyr Ala Leu Pro Val Gln Gln Asn Met Thr Arg Ile Ile Phe	
340 345 350	
gga gat ctt att ggc cct gta gaa act gtg cct cag gtt ccc cgc caa	1104
Gly Asp Leu Ile Gly Pro Val Glu Thr Val Pro Gln Val Pro Arg Gln	
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Asn Ser Asp Asn Phe His Phe Asn Leu Ser Asp Val Tyr Arg Asn Pro	
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Leu Pro Asn Asn Asp Ile Phe Asn Tyr Arg Tyr Gly Gly Leu Gln Ile	
385 390 395 400	
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Ser Lys Ala Gln Phe Met Thr Tyr Tyr Lys Lys Phe Gly Ala Phe Ser	
405 410 415	
acc cat gat gaa tat tat tat gta gat ggg cat cgc cta agt ttt aat	1296
Thr His Asp Glu Tyr Tyr Tyr Val Asp Gly His Arg Leu Ser Phe Asn	
420 425 430	
act tca gat aaa aaa aca att gaa atc aat gct cat caa aat tct cat	1344
Thr Ser Asp Lys Lys Thr Ile Glu Ile Asn Ala His Gln Asn Ser His	
435 440 445	
gat act att gaa aag gat gta ata gat caa cta ggc ggc tat gtt aca	1392
Asp Thr Ile Glu Lys Asp Val Ile Asp Gln Leu Gly Gly Tyr Val Thr	
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Arg Met Asn Met Val Ser Gln Glu Ile Gly Ser Gly Ser Ile Leu Gly	
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Gly Asn Ala Ile Asp Arg Thr Ala Leu Thr Thr Ser Thr Gly Asp Lys	
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Asp Ile Leu Ala Ala Gly Phe Asn Ala Ile Asn Asn Gly Asn Tyr Lys	
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aca gaa ggt cgc ggt gcc tcc cat aat cag gat gtt cca aat cat aaa	1584
Thr Glu Gly Arg Gly Ala Ser His Asn Gln Asp Val Pro Asn His Lys	
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gtt caa gcg att tat cct gtt caa ccg aat aaa tat gaa tat gac gat	1632
Val Gln Ala Ile Tyr Pro Val Gln Pro Asn Lys Tyr Glu Tyr Asp Asp	
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tat gga tct gaa gaa aag tat gga tac ctt tat act tta att cca atg	1680
Tyr Gly Ser Glu Glu Lys Tyr Gly Tyr Leu Tyr Thr Leu Ile Pro Met	
545 550 555 560	
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Asp Val Ser Phe Ile Pro Gln Leu Asn Ala Glu Asp Val Ile Thr Thr	
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att cct gca gaa caa gca gtc aaa att aat ggt caa tct gta ata gat	1776
Ile Pro Ala Glu Gln Ala Val Lys Ile Asn Gly Gln Ser Val Ile Asp	
580 585 590	
act gta aac acc aat tct tta ttg gaa ttt gtt aat ggt gca aat gca	1824
Thr Val Asn Thr Asn Ser Leu Leu Glu Phe Val Asn Gly Ala Asn Ala	
595 600 605	
att aaa cta tct cct ggc gaa aca gca caa tac act atg att aat ccc	1872
Ile Lys Leu Ser Pro Gly Glu Thr Ala Gln Tyr Thr Met Ile Asn Pro	
610 615 620	
gtc aat cgt tcc tac cag gtt aga gtt cgg gtt gct act gaa gga gaa	1920
Val Asn Arg Ser Tyr Gln Val Arg Val Arg Val Ala Thr Glu Gly Glu	
625 630 635 640	

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acc caa tta gat att ata gca ccc gtt gat agc aat acc ctt aat ctt	1968
Thr Gln Leu Asp Ile Ile Ala Pro Val Asp Ser Asn Thr Leu Asn Leu	
645 650 655	
tca aac aca aaa aca aca gca aat gat caa aat ggg ata tta ggt aaa	2016
Ser Asn Thr Lys Thr Thr Ala Asn Asp Gln Asn Gly Ile Leu Gly Lys	
660 665 670	
caa ggt aat tat ata gta ttt cca cag cca aac att gat act gtc aca	2064
Gln Gly Asn Tyr Ile Val Phe Pro Gln Pro Asn Ile Asp Thr Val Thr	
675 680 685	
ggc acc agt tta cct cct acc gaa aac att atg aat ttt cca gta gga	2112
Gly Thr Ser Leu Pro Pro Thr Glu Asn Ile Met Asn Phe Pro Val Gly	
690 695 700	
aca ttt gat ttt acc att gta aat tct gga aac tca gat act att tta	2160
Thr Phe Asp Phe Thr Ile Val Asn Ser Gly Asn Ser Asp Thr Ile Leu	
705 710 715 720	
gat cga att gaa ttt gtt cct att gta act tct aat aaa att caa caa	2208
Asp Arg Ile Glu Phe Val Pro Ile Val Thr Ser Asn Lys Ile Gln Gln	
725 730 735	
gat ttc act att tct cct gga aca agt caa gta att tgg acc gga aat	2256
Asp Phe Thr Ile Ser Pro Gly Thr Ser Gln Val Ile Trp Thr Gly Asn	
740 745 750	
tca gct aac act ata gat att aca att att gac aac gta gat aca agc	2304
Ser Ala Asn Thr Ile Asp Ile Thr Ile Ile Asp Asn Val Asp Thr Ser	
755 760 765	
ggg tta ttc gtt caa att ttc caa aaa ggt aag caa ctg cat gga gaa	2352
Gly Leu Phe Val Gln Ile Phe Gln Lys Gly Lys Gln Leu His Gly Glu	
770 775 780	
cta act ttg att gat ccc gct cat att caa cgt aca ttc tct gaa aaa	2400
Leu Thr Leu Ile Asp Pro Ala His Ile Gln Arg Thr Phe Ser Glu Lys	
785 790 795 800	
ttt gat caa att gtt ttg tat aac cca ggt tat aat agt tct ata tct	2448
Phe Asp Gln Ile Val Leu Tyr Asn Pro Gly Tyr Asn Ser Ser Ile Ser	
805 810 815	
ggg aca gtg agt ggt tca gta agc tct att cct aag aaa ttc gaa tta	2496
Gly Thr Val Ser Gly Ser Val Ser Ser Ile Pro Lys Lys Phe Glu Leu	
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tct agc gac tta caa aat atc aca aac caa gtt aat aac tta ttt gca	2544
Ser Ser Asp Leu Gln Asn Ile Thr Asn Gln Val Asn Asn Leu Phe Ala	
835 840 845	
tcg agc gaa cat gat aca ctt gcc aca gat gta agt gat tat gat att	2592
Ser Ser Glu His Asp Thr Leu Ala Thr Asp Val Ser Asp Tyr Asp Ile	
850 855 860	
gaa gaa gtg att cta aaa gta gat gca tta tct gat gaa gtg ttt gga	2640
Glu Glu Val Ile Leu Lys Val Asp Ala Leu Ser Asp Glu Val Phe Gly	
865 870 875 880	
aaa gag aaa aaa gca cta cgt aaa ttg gta aat caa gcg aag cgt tta	2688
Lys Glu Lys Lys Ala Leu Arg Lys Leu Val Asn Gln Ala Lys Arg Leu	
885 890 895	
agt aaa gcg cgt aat ctt ctc cta gga gga agt ttt gat aat ttg gat	2736
Ser Lys Ala Arg Asn Leu Leu Leu Gly Gly Ser Phe Asp Asn Leu Asp	
900 905 910	
gct tgg tat agg gga cga aat gta gta act gta tct gat cat gaa ctg	2784
Ala Trp Tyr Arg Gly Arg Asn Val Val Thr Val Ser Asp His Glu Leu	
915 920 925	
ttt aaa agt gat cat ata tta tta cca cta cca aca aca ttg tat cca	2832
Phe Lys Ser Asp His Ile Leu Leu Pro Leu Pro Thr Thr Leu Tyr Pro	
930 935 940	

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cgt tat act gtc tct ggt ttc atc gcg cat gca gag gat tta gaa att Arg Tyr Thr Val Ser Gly Phe Ile Ala His Ala Glu Asp Leu Glu Ile 965 970 975	2928
gtt gtt tct cgt tat ggg caa gaa ata aag aaa gtg gtg caa gtt cca Val Val Ser Arg Tyr Gly Gln Glu Ile Lys Lys Val Val Gln Val Pro 980 985 990	2976
tat ggt gaa gca ttc cca ttg aca tcg agc gga cca att tgt tgt aga Tyr Gly Glu Ala Phe Pro Leu Thr Ser Ser Gly Pro Ile Cys Cys Arg 995 1000 1005	3024
cca cgt tct aga gta aat ggt aaa cct gct gat cca cat ttc ttt agt Pro Arg Ser Arg Val Asn Gly Lys Pro Ala Asp Pro His Phe Phe Ser 1010 1015 1020	3072
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aag gtg caa cgt gct gct aga gat tgg aaa caa aag tat gat caa gag Lys Val Gln Arg Ala Ala Arg Asp Trp Lys Gln Lys Tyr Asp Gln Glu 1075 1080 1085	3264
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gcg ttg tat gaa aat gaa gat tgg aat gga gca att cgt tct gga gtt Ala Leu Tyr Glu Asn Glu Asp Trp Asn Gly Ala Ile Arg Ser Gly Val 1105 1110 1115 1120	3360
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agt aca att ctg cat aat ggc cat ttc aca aca gat gca gca aat tgg Ser Thr Ile Leu His Asn Gly His Phe Thr Thr Asp Ala Ala Asn Trp 1170 1175 1180	3552
acg ata gaa ggc gat gca cat cag gta gta tta gaa gat ggt aga cgt Thr Ile Glu Gly Asp Ala His Gln Val Val Leu Glu Asp Gly Arg Arg 1185 1190 1195 1200	3600
gta tta cga ttg cca gat tgg tct tcg agt ttg tct caa acg att gaa Val Leu Arg Leu Pro Asp Trp Ser Ser Leu Ser Gln Thr Ile Glu 1205 1210 1215	3648
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caa gga gaa gga acg gtt acg ttg gag cat ggt gaa gaa gga gaa tat Gln Gly Glu Gly Thr Val Thr Leu Glu His Gly Glu Glu Gly Glu Tyr 1235 1240 1245	3744

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Val Glu Thr His Pro His Lys Phe Ala Asn Phe Thr Thr Ser Gln Arg	
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caa gga att acg ttt gaa tca aat aaa gtg aca gtg act att tct tca	3840
Gln Gly Ile Thr Phe Glu Ser Asn Lys Val Thr Val Thr Ile Ser Ser	
1265 1270 1275 1280	
gaa gat gga gaa ttc tta gcg gat aat att gca att gtg gaa gtt cct	3888
Glu Asp Gly Glu Phe Leu Ala Asp Asn Ile Ala Ile Val Glu Val Pro	
1285 1290 1295	
atg ttt aac aag aat caa atg gtc aat gaa aat aga ggt gta aat ata	3936
Met Phe Asn Lys Asn Gln Met Val Asn Glu Asn Arg Gly Val Asn Ile	
1300 1305 1310	
aat agc aat aca aat atg aat agt agc aat aac agc aat aac caa taa	3984
Asn Ser Asn Thr Asn Met Asn Ser Ser Asn Asn Ser Asn Asn Gln *	
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<210> SEQ ID NO 4

<211> LENGTH: 1327

<212> TYPE: PRT

<213> ORGANISM: Unknown

<220> FEATURE:

<223> OTHER INFORMATION: Isolated from soil sample

<400> SEQUENCE: 4

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20 25 30	
Lys Ile Glu Glu Gly Ile Lys Glu Phe Glu Lys Thr Gly Arg Ile Lys	
35 40 45	
Pro Leu Lys Asp Leu Ile Glu Leu Ile Phe Lys Gly Tyr Ser Asp Asp	
50 55 60	
Glu Ser Ser Tyr Ala Ala Leu Val Gln Thr Met Leu Val Val Ile Pro	
65 70 75 80	
Leu Ala Phe Pro Glu Leu Ala Pro Val Leu Pro Ile Ile Gly Val Val	
85 90 95	
Ile Asn Phe Val Phe Pro Gly Leu Lys Gly Ser Ala Lys Ser Thr Tyr	
100 105 110	
Thr Met Ile Thr Glu Met Val Asp Lys Ala Ile Asn Gln Ser Phe Thr	
115 120 125	
Ala Gln Ile Thr Asn Ile Leu Thr Asn Asn Ile Thr Gly Ile Gln Asn	
130 135 140	
Asn Ile Gln Ser Val Tyr Asp Ala Met Ser Asn Ala Ile Gly Thr Asn	
145 150 155 160	
Asp Thr Ile His Asn Phe Ile Arg Asn Asn Asp Thr Thr Pro Cys Ser	
165 170 175	
Gln Asn Asn Gln Pro Ala Cys Pro Cys Pro Pro Asn Asn Gln Cys Leu	
180 185 190	
Gln Lys Val Val Asp Glu Tyr Thr Lys Ala Ile Ala Asn Ile Asp Leu	
195 200 205	
Ile Ile Pro Gln Phe His Asp Pro Leu Thr Gly Val Ile Ser Asp Leu	
210 215 220	
Ala Thr Ala Asn Met Tyr Ile Leu Pro Leu Tyr Ala Gln Thr Val Asn	
225 230 235 240	
Leu Lys Leu Ile Leu Arg Gln Ser Phe Ile Glu Phe Met Glu Lys Tyr	

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245								250				255			
Lys	Tyr	Asp	Glu	Lys	Glu	Thr	Val	Phe	Gln	Ala	Phe	Ile	Asn	Ala	Asp
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Ile	Pro	Glu	Gln	Ile	Lys	Lys	Leu	Arg	Gln	Asp	Ile	Ile	Thr	Tyr	Thr
			275				280					285			
Lys	Asp	Ile	Tyr	Met	Gln	Phe	Glu	Ala	His	Ala	Pro	Tyr	Pro	Thr	Tyr
			290			295					300				
Asn	Ser	Lys	Lys	Gln	Leu	Asn	Asp	Tyr	Ile	Arg	Tyr	Thr	Arg	Ile	Ile
305					310					315					320
Gln	Val	Tyr	Cys	Leu	Asp	Leu	Val	Ala	Met	Trp	Pro	Thr	Leu	Asp	Arg
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Val	Asn	Tyr	Ala	Leu	Pro	Val	Gln	Gln	Asn	Met	Thr	Arg	Ile	Ile	Phe
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Gly	Asp	Leu	Ile	Gly	Pro	Val	Glu	Thr	Val	Pro	Gln	Val	Pro	Arg	Gln
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Asn	Ser	Asp	Asn	Phe	His	Phe	Asn	Leu	Ser	Asp	Val	Tyr	Arg	Asn	Pro
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Leu	Pro	Asn	Asn	Asp	Ile	Phe	Asn	Tyr	Arg	Tyr	Gly	Gly	Leu	Gln	Ile
385					390					395					400
Ser	Lys	Ala	Gln	Phe	Met	Thr	Tyr	Tyr	Lys	Lys	Phe	Gly	Ala	Phe	Ser
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Thr	His	Asp	Glu	Tyr	Tyr	Tyr	Val	Asp	Gly	His	Arg	Leu	Ser	Phe	Asn
			420					425					430		
Thr	Ser	Asp	Lys	Lys	Thr	Ile	Glu	Ile	Asn	Ala	His	Gln	Asn	Ser	His
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Asp	Thr	Ile	Glu	Lys	Asp	Val	Ile	Asp	Gln	Leu	Gly	Gly	Tyr	Val	Thr
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Arg	Met	Asn	Met	Val	Ser	Gln	Glu	Ile	Gly	Ser	Gly	Ser	Ile	Leu	Gly
465					470					475					480
Gly	Asn	Ala	Ile	Asp	Arg	Thr	Ala	Leu	Thr	Thr	Ser	Thr	Gly	Asp	Lys
				485					490					495	
Asp	Ile	Leu	Ala	Ala	Gly	Phe	Asn	Ala	Ile	Asn	Asn	Gly	Asn	Tyr	Lys
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Val	Gln	Ala	Ile	Tyr	Pro	Val	Gln	Pro	Asn	Lys	Tyr	Glu	Tyr	Asp	Asp
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Tyr	Gly	Ser	Glu	Glu	Lys	Tyr	Gly	Tyr	Leu	Tyr	Thr	Leu	Ile	Pro	Met
545					550					555					560
Asp	Val	Ser	Phe	Ile	Pro	Gln	Leu	Asn	Ala	Glu	Asp	Val	Ile	Thr	Thr
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Ile	Pro	Ala	Glu	Gln	Ala	Val	Lys	Ile	Asn	Gly	Gln	Ser	Val	Ile	Asp
			580					585					590		
Thr	Val	Asn	Thr	Asn	Ser	Leu	Leu	Glu	Phe	Val	Asn	Gly	Ala	Asn	Ala
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Ile	Lys	Leu	Ser	Pro	Gly	Glu	Thr	Ala	Gln	Tyr	Thr	Met	Ile	Asn	Pro
						615					620				
Val	Asn	Arg	Ser	Tyr	Gln	Val	Arg	Val	Arg	Val	Ala	Thr	Glu	Gly	Glu
625					630					635					640
Thr	Gln	Leu	Asp	Ile	Ile	Ala	Pro	Val	Asp	Ser	Asn	Thr	Leu	Asn	Leu
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Ser	Asn	Thr	Lys	Thr	Thr	Ala	Asn	Asp	Gln	Asn	Gly	Ile	Leu	Gly	Lys
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Gly	Thr	Ser	Leu	Pro	Pro	Thr	Glu	Asn	Ile	Met	Asn	Phe	Pro	Val	Gly
	690					695					700				
Thr	Phe	Asp	Phe	Thr	Ile	Val	Asn	Ser	Gly	Asn	Ser	Asp	Thr	Ile	Leu
705					710					715					720
Asp	Arg	Ile	Glu	Phe	Val	Pro	Ile	Val	Thr	Ser	Asn	Lys	Ile	Gln	Gln
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Phe	Asp	Gln	Ile	Val	Leu	Tyr	Asn	Pro	Gly	Tyr	Asn	Ser	Ser	Ile	Ser
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Gly	Thr	Val	Ser	Gly	Ser	Val	Ser	Ser	Ile	Pro	Lys	Lys	Phe	Glu	Leu
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865					870					875					880
Lys	Glu	Lys	Lys	Ala	Leu	Arg	Lys	Leu	Val	Asn	Gln	Ala	Lys	Arg	Leu
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Ser	Lys	Ala	Arg	Asn	Leu	Leu	Leu	Gly	Gly	Ser	Phe	Asp	Asn	Leu	Asp
		900						905					910		
Ala	Trp	Tyr	Arg	Gly	Arg	Asn	Val	Val	Thr	Val	Ser	Asp	His	Glu	Leu
		915				920						925			
Phe	Lys	Ser	Asp	His	Ile	Leu	Leu	Pro	Leu	Pro	Thr	Thr	Leu	Tyr	Pro
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945					950					955					960
Arg	Tyr	Thr	Val	Ser	Gly	Phe	Ile	Ala	His	Ala	Glu	Asp	Leu	Glu	Ile
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Glu	Leu	Gly	Phe	Arg	Ile	Val	Glu	Pro	Thr	Gly	Met	Ala	Arg	Val	Ser
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Lys Val Gln Arg Ala Ala Arg Asp Trp Lys Gln Lys Tyr Asp Gln Glu
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Arg Ala Glu Val Arg Ala Leu Ile Gln Pro Val Leu Asn Gln Ile Asn
      1090                      1095                      1100

Ala Leu Tyr Glu Asn Glu Asp Trp Asn Gly Ala Ile Arg Ser Gly Val
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Ser Tyr His Asp Leu Glu Ala Ile Val Leu Pro Thr Leu Pro Lys Leu
      1125                      1130                      1135

Asn His Trp Phe Met Ser Asp Met Leu Gly Glu Gln Gly Ser Ile Leu
      1140                      1145                      1150

Ala Gln Phe Gln Glu Ala Leu Asn Arg Ala Tyr Thr Gln Leu Glu Gly
      1155                      1160                      1165

Ser Thr Ile Leu His Asn Gly His Phe Thr Thr Asp Ala Ala Asn Trp
      1170                      1175                      1180

Thr Ile Glu Gly Asp Ala His Gln Val Val Leu Glu Asp Gly Arg Arg
      1185                      1190                      1195                      1200

Val Leu Arg Leu Pro Asp Trp Ser Ser Ser Leu Ser Gln Thr Ile Glu
      1205                      1210                      1215

Ile Glu Asn Phe Asp Pro Asp Lys Glu Tyr Gln Leu Val Phe His Gly
      1220                      1225                      1230

Gln Gly Glu Gly Thr Val Thr Leu Glu His Gly Glu Glu Gly Glu Tyr
      1235                      1240                      1245

Val Glu Thr His Pro His Lys Phe Ala Asn Phe Thr Thr Ser Gln Arg
      1250                      1255                      1260

Gln Gly Ile Thr Phe Glu Ser Asn Lys Val Thr Val Thr Ile Ser Ser
      1265                      1270                      1275                      1280

Glu Asp Gly Glu Phe Leu Ala Asp Asn Ile Ala Ile Val Glu Val Pro
      1285                      1290                      1295

Met Phe Asn Lys Asn Gln Met Val Asn Glu Asn Arg Gly Val Asn Ile
      1300                      1305                      1310

Asn Ser Asn Thr Asn Met Asn Ser Ser Asn Asn Ser Asn Asn Gln
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<210> SEQ ID NO 5
<211> LENGTH: 3720
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Isolated from soil sample
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<221> NAME/KEY: CDS
<222> LOCATION: (1)...(3720)

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  1           5           10           15

aat gtg tta gca act cca aat gtc tta gca aca aac aaa caa cca cta      96
Asn Val Leu Ala Thr Pro Asn Val Leu Ala Thr Asn Lys Gln Pro Leu
      20           25           30

gca gat aca gat gca tta aat aaa ttt tac aac gat ttg caa att gga      144
Ala Asp Thr Asp Ala Leu Asn Lys Phe Tyr Asn Asp Leu Gln Ile Gly
      35           40           45

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aaa gtt tca gct ttt aca att gat gca tta tgg agc ctt atg aca acc	192
Lys Val Ser Ala Phe Thr Ile Asp Ala Leu Trp Ser Leu Met Thr Thr	
50 55 60	
gga aaa tat gac tgg tcg tca att gct aaa ttt tgt tgg tct ctt gga	240
Gly Lys Tyr Asp Trp Ser Ser Ile Ala Lys Phe Cys Trp Ser Leu Gly	
65 70 75 80	
act ggt gta aca cct ctg tta ggt ata ttt tca cct att ata gat ata	288
Thr Gly Val Thr Pro Leu Leu Gly Ile Phe Ser Pro Ile Ile Asp Ile	
85 90 95	
att ttc cct gct tta ttc ggt ggt aac aaa cta agt cta ttt gaa caa	336
Ile Phe Pro Ala Leu Phe Gly Gly Asn Lys Leu Ser Leu Phe Glu Gln	
100 105 110	
cta aaa cct caa ata gaa aaa ctg att att gaa aaa tta aca gat gaa	384
Leu Lys Pro Gln Ile Glu Lys Leu Ile Ile Glu Lys Leu Thr Asp Glu	
115 120 125	
gaa aaa aat ttc tta gct caa aaa act agt gat att caa tcc tat tta	432
Glu Lys Asn Phe Leu Ala Gln Lys Thr Ser Asp Ile Gln Ser Tyr Leu	
130 135 140	
aat gat tat aaa agt gca gtt tct aaa att aat aat cca aat gtt ata	480
Asn Asp Tyr Lys Ser Ala Val Ser Lys Ile Asn Asn Pro Asn Val Ile	
145 150 155 160	
gat agc gat ttt gaa tct tta cat gca aca att aat cta aca tta tca	528
Asp Ser Asp Phe Glu Ser Leu His Ala Thr Ile Asn Leu Thr Leu Ser	
165 170 175	
aaa ata aaa gga tca tta tct tat ttc tct atc ttt aac cag cca gat	576
Lys Ile Lys Gly Ser Leu Ser Tyr Phe Ser Ile Phe Asn Gln Pro Asp	
180 185 190	
gat aga aaa cca att tat aca ata cta ggt tta cct tat tat acc ctt	624
Asp Arg Lys Pro Ile Tyr Thr Ile Leu Gly Leu Pro Tyr Tyr Thr Leu	
195 200 205	
atg gcc act atg tat tta aca tta tta cga gac gtt att tta aat aca	672
Met Ala Thr Met Tyr Leu Thr Leu Leu Arg Asp Val Ile Leu Asn Thr	
210 215 220	
aca aaa tgg aaa ata tca cca gct tct aat att tcc tat cgt caa caa	720
Thr Lys Trp Lys Ile Ser Pro Ala Ser Asn Ile Ser Tyr Arg Gln Gln	
225 230 235 240	
ttt aaa caa aac atg aat tca ttt gtt ctt aca att aaa aat aat tat	768
Phe Lys Gln Asn Met Asn Ser Phe Val Leu Thr Ile Lys Asn Asn Tyr	
245 250 255	
caa act ggt ttt aat tat ata aca aat gaa gct tac aaa gca cat cct	816
Gln Thr Gly Phe Asn Tyr Ile Thr Asn Glu Ala Tyr Lys Ala His Pro	
260 265 270	
aca aat cct tca aag act ata ctt cca ttt gaa aat aaa atg aca ttg	864
Thr Asn Pro Ser Lys Thr Ile Leu Pro Phe Glu Asn Lys Met Thr Leu	
275 280 285	
gac tgt ttt gac tat gtt gca atg tgg ccc act tta tat cca gat gat	912
Asp Cys Phe Asp Tyr Val Ala Met Trp Pro Thr Leu Tyr Pro Asp Asp	
290 295 300	
tat tat act gaa aaa aca aat ttg caa aaa act cgc tta tta ttt tcc	960
Tyr Tyr Thr Glu Lys Thr Asn Leu Gln Lys Thr Arg Leu Leu Phe Ser	
305 310 315 320	
cca ata tta ggt cgt atg cca gat tct cga agt caa tgg ctt cat agt	1008
Pro Ile Leu Gly Arg Met Pro Asp Ser Arg Ser Gln Trp Leu His Ser	
325 330 335	
aaa cct tat tcc tgg gat agt aat aaa act ttt acg ttc gat cac tat	1056
Lys Pro Tyr Ser Trp Asp Ser Asn Lys Thr Phe Thr Phe Asp His Tyr	
340 345 350	

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tat atg gct gaa ctc aca cac att gac act aaa gaa ttt gat cga gta Tyr Met Ala Glu Leu Thr His Ile Asp Thr Lys Glu Phe Asp Arg Val 355 360 365	1104
gac aga atc cgt cag att tat caa gaa gga tat caa aaa gaa caa caa Asp Arg Ile Arg Gln Ile Tyr Gln Glu Gly Tyr Gln Lys Glu Gln Gln 370 375 380	1152
acg tat gat gat tat tac act tat ggc gga gat tct gct caa aat act Thr Tyr Asp Asp Tyr Tyr Thr Tyr Gly Gly Asp Ser Ala Gln Asn Thr 385 390 395 400	1200
tct ttt aca aca gat aat cca ctt gca atc atg tat cct act cga ggt Ser Phe Thr Thr Asp Asn Pro Leu Ala Ile Met Tyr Pro Thr Arg Gly 405 410 415	1248
ggt aat tat gta ggt acc gct att aaa tgg ttt gat gac aca gtg caa Gly Asn Tyr Val Gly Thr Ala Ile Lys Trp Phe Asp Asp Thr Val Gln 420 425 430	1296
ggt ggt cga tct tca gga tat aca act cca tat tct gga gac cct gat Gly Gly Arg Ser Ser Gly Tyr Thr Thr Pro Tyr Ser Gly Asp Pro Asp 435 440 445	1344
cct ata ata act cct gat gat cat aaa gtt aat ttt ctc tat aca gta Pro Ile Ile Thr Pro Asp Asp His Lys Val Asn Phe Leu Tyr Thr Val 450 455 460	1392
aaa gat gaa tta aaa gga att gat gca tgg gtc aat tca tgg gtt ccc Lys Asp Glu Leu Lys Gly Ile Asp Ala Trp Val Asn Ser Trp Val Pro 465 470 475 480	1440
att tat aca act gtt cca aat ata att gaa aat gaa atg ttc ctc act Ile Tyr Thr Thr Val Pro Asn Ile Ile Glu Asn Glu Met Phe Leu Thr 485 490 495	1488
aca cta ggt ttt cct ttt gaa aaa gga ata att gat aca ggc gga gct Thr Leu Gly Phe Pro Phe Glu Lys Gly Ile Ile Asp Thr Gly Gly Ala 500 505 510	1536
ggt gga gat aaa ata tat caa cta gaa cga tta aat gga tcc atg gct Gly Gly Asp Lys Ile Tyr Gln Leu Glu Arg Leu Asn Gly Ser Met Ala 515 520 525	1584
atc aac tta aaa ttt aaa caa ata att aaa tta cca ttt aca aat cta Ile Asn Leu Lys Phe Lys Gln Ile Ile Lys Leu Pro Phe Thr Asn Leu 530 535 540	1632
aca acc ggt aat tat cta att cgt tta cgt tat gca agt cat tcg gat Thr Thr Gly Asn Tyr Leu Ile Arg Leu Arg Tyr Ala Ser His Ser Asp 545 550 555 560	1680
ata aat gca ttt act cac att cac tct gaa aat gga gct gat atc agc Ile Asn Ala Phe Thr His Ile His Ser Glu Asn Gly Ala Asp Ile Ser 565 570 575	1728
agt act cct tta gga aat att act ctt cct aac acg caa aat ttc act Ser Thr Pro Leu Gly Asn Ile Thr Leu Pro Asn Thr Gln Asn Phe Thr 580 585 590	1776
ttt cct act aac gat gaa tac caa ccc aat caa ccc caa tat acg acc Phe Pro Thr Asn Asp Glu Tyr Gln Pro Asn Gln Pro Gln Tyr Thr Thr 595 600 605	1824
tat ata gag gga aat gct ggt aaa tat gct tta tat caa ttt aca caa Tyr Ile Glu Gly Asn Ala Gly Lys Tyr Ala Leu Tyr Gln Phe Thr Gln 610 615 620	1872
aat atc tcg ctc aca tct gga caa tat act ttc tat att caa aat aat Asn Ile Ser Leu Thr Ser Gly Gln Tyr Thr Phe Tyr Ile Gln Asn Asn 625 630 635 640	1920
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gaa att tgg aaa agt gat cgt cca tat ggc cat tct ata aat gga ata	2064
Glu Ile Trp Lys Ser Asp Arg Pro Tyr Gly His Ser Ile Asn Gly Ile	
675 680 685	
ttc ata gtc agc gtg cca ttt gga aac cag aca gat act gta act ata	2112
Phe Ile Val Ser Val Pro Phe Gly Asn Gln Thr Asp Thr Val Thr Ile	
690 695 700	
aca tat tgg aat aat ggg gaa aaa gtc cat aca gac tct caa aca ttt	2160
Thr Tyr Trp Asn Asn Gly Glu Lys Val His Thr Asp Ser Gln Thr Phe	
705 710 715 720	
gat atg gca aga ttc caa ggt caa gat ctt aca caa tgg caa gga gct	2208
Asp Met Ala Arg Phe Gln Gly Gln Asp Leu Thr Gln Trp Gln Gly Ala	
725 730 735	
ttt gat cgt gta act att cgt aga act cat tct gat ggt aca ttg tca	2256
Phe Asp Arg Val Thr Ile Arg Arg Thr His Ser Asp Gly Thr Leu Ser	
740 745 750	
tta aca agt gca acc cta tac ttt gtt atc cca aaa tca tcc ttt agt	2304
Leu Thr Ser Ala Thr Leu Tyr Phe Val Ile Pro Lys Ser Ser Phe Ser	
755 760 765	
acc cca gaa gat tta gaa aaa atc aca aac caa gtc aat cag tta ttt	2352
Thr Pro Glu Asp Leu Glu Lys Ile Thr Asn Gln Val Asn Gln Leu Phe	
770 775 780	
act tcc tca tcc caa aca gaa tta gct aac acc gta acc gat tac gga	2400
Thr Ser Ser Ser Gln Thr Glu Leu Ala Asn Thr Val Thr Asp Tyr Gly	
785 790 795 800	
att gat caa gtt ttg atg aaa gta gat gcg tta tca gac gat gta ttt	2448
Ile Asp Gln Val Leu Met Lys Val Asp Ala Leu Ser Asp Asp Val Phe	
805 810 815	
ggg gta gag aaa aaa gca tta cgt aaa ctt gtc aat cag gcc aaa caa	2496
Gly Val Glu Lys Lys Ala Leu Arg Lys Leu Val Asn Gln Ala Lys Gln	
820 825 830	
ctg agt aaa gca cgc aat gta tta gtc ggt gga aac ttt gaa gga aat	2544
Leu Ser Lys Ala Arg Asn Val Leu Val Gly Gly Asn Phe Glu Gly Asn	
835 840 845	
cat gaa tgg gta ctc ggt cgt aaa gcg gtc atg gtc gca aat gat gag	2592
His Glu Trp Val Leu Gly Arg Lys Ala Val Met Val Ala Asn Asp Glu	
850 855 860	
tta ttt aaa ggc aat cat tta tta tta cca cct cca agt cta tat cca	2640
Leu Phe Lys Gly Asn His Leu Leu Leu Pro Pro Pro Ser Leu Tyr Pro	
865 870 875 880	
tcg tat gcg tat caa aaa gtg gat gaa tcc aaa tta aaa ccg aat aca	2688
Ser Tyr Ala Tyr Gln Lys Val Asp Glu Ser Lys Leu Lys Pro Asn Thr	
885 890 895	
cga tat acc gtt tct ggt ttt gtg gcg caa agt gaa caa tta gaa gtc	2736
Arg Tyr Thr Val Ser Gly Phe Val Ala Gln Ser Glu Gln Leu Glu Val	
900 905 910	
gtt gtt tcc cgt tat ggt aaa gaa gta cat gac atg tta aat gtt cct	2784
Val Val Ser Arg Tyr Gly Lys Glu Val His Asp Met Leu Asn Val Pro	
915 920 925	
tat gaa gaa gcg tta ccg att tct tca aat gaa aag tca aat tgt tgt	2832
Tyr Glu Glu Ala Leu Pro Ile Ser Ser Asn Glu Lys Ser Asn Cys Cys	
930 935 940	
aaa ccg gct act tgc aac tat aca tct tgt gag ggg aaa gaa cca gat	2880
Lys Pro Ala Thr Cys Asn Tyr Thr Ser Cys Glu Gly Lys Glu Pro Asp	
945 950 955 960	

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gca aat cta gga att gaa ttc ggt ctt cgt att gtg aaa tca aat gga	2976
Ala Asn Leu Gly Ile Glu Phe Gly Leu Arg Ile Val Lys Ser Asn Gly	
980 985 990	
ttt gca aaa atc agt aat tta gaa atc aaa gaa gat cgt cca tta aca	3024
Phe Ala Lys Ile Ser Asn Leu Glu Ile Lys Glu Asp Arg Pro Leu Thr	
995 1000 1005	
gac caa gaa att aaa aaa gta caa cac aaa gaa caa aag tgg aaa aaa	3072
Asp Gln Glu Ile Lys Lys Val Gln His Lys Glu Gln Lys Trp Lys Lys	
1010 1015 1020	
gca ttt aac aaa gaa caa gca gag tta acg gca aca ctc caa cca aca	3120
Ala Phe Asn Lys Glu Gln Ala Glu Leu Thr Ala Thr Leu Gln Pro Thr	
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ctg aat caa atc aat gcc ttg tat caa cag gaa gat tgg aat ggt tcg	3168
Leu Asn Gln Ile Asn Ala Leu Tyr Gln Gln Glu Asp Trp Asn Gly Ser	
1045 1050 1055	
att cat cct cat gtg acg tat caa cat ctg tct gat gtt gtc tta cca	3216
Ile His Pro His Val Thr Tyr Gln His Leu Ser Asp Val Val Leu Pro	
1060 1065 1070	
acg tta cca aaa caa aca cat tgg ttt atg gaa aat cga gaa ggc gaa	3264
Thr Leu Pro Lys Gln Thr His Trp Phe Met Glu Asn Arg Glu Gly Glu	
1075 1080 1085	
cat gtt gtt ctg acg caa caa ttc caa caa gca tta gat cgt gct ttc	3312
His Val Val Leu Thr Gln Gln Phe Gln Gln Ala Leu Asp Arg Ala Phe	
1090 1095 1100	
caa caa atc gaa gaa caa aac ttg atc cac aat ggt agc ttt aca agt	3360
Gln Gln Ile Glu Glu Gln Asn Leu Ile His Asn Gly Ser Phe Thr Ser	
1105 1110 1115 1120	
gga tta aca gat tgg act gta aca gga gat gca cag att act atc tat	3408
Gly Leu Thr Asp Trp Thr Val Thr Gly Asp Ala Gln Ile Thr Ile Tyr	
1125 1130 1135	
gat gaa gat cca gta tta gaa cta gca cat tgg gat gca agc gtc tct	3456
Asp Glu Asp Pro Val Leu Glu Leu Ala His Trp Asp Ala Ser Val Ser	
1140 1145 1150	
caa acg att gag att act gat ttt gaa gaa gaa aaa gaa tac aaa ctt	3504
Gln Thr Ile Glu Ile Thr Asp Phe Glu Glu Glu Lys Glu Tyr Lys Leu	
1155 1160 1165	
cgt gta cgc gga aaa ggc aaa gga acg gtt acc gtt caa cat gaa gaa	3552
Arg Val Arg Gly Lys Gly Lys Gly Thr Val Thr Val Gln His Glu Glu	
1170 1175 1180	
gag tta gaa aca atg aca ttt aac aca act agt ttt aca acg aaa gaa	3600
Glu Leu Glu Thr Met Thr Phe Asn Thr Thr Ser Phe Thr Thr Lys Glu	
1185 1190 1195 1200	
caa acc ttc tat ttc gaa gga aat aca ata gat gta cac gtt caa tca	3648
Gln Thr Phe Tyr Phe Glu Gly Asn Thr Ile Asp Val His Val Gln Ser	
1205 1210 1215	
gag aat aat gca ttc ctt gta gac agt gtg gaa ctc att gaa gtt gta	3696
Glu Asn Asn Ala Phe Leu Val Asp Ser Val Glu Leu Ile Glu Val Val	
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<210> SEQ ID NO 6

<211> LENGTH: 1239

<212> TYPE: PRT

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<213> ORGANISM: Unknown

<220> FEATURE:

<223> OTHER INFORMATION: Isolated from soil sample

<400> SEQUENCE: 6

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 20          25          30

Ala Asp Thr Asp Ala Leu Asn Lys Phe Tyr Asn Asp Leu Gln Ile Gly
 35          40          45

Lys Val Ser Ala Phe Thr Ile Asp Ala Leu Trp Ser Leu Met Thr Thr
 50          55          60

Gly Lys Tyr Asp Trp Ser Ser Ile Ala Lys Phe Cys Trp Ser Leu Gly
 65          70          75          80

Thr Gly Val Thr Pro Leu Leu Gly Ile Phe Ser Pro Ile Ile Asp Ile
 85          90          95

Ile Phe Pro Ala Leu Phe Gly Gly Asn Lys Leu Ser Leu Phe Glu Gln
100          105          110

Leu Lys Pro Gln Ile Glu Lys Leu Ile Ile Glu Lys Leu Thr Asp Glu
115          120          125

Glu Lys Asn Phe Leu Ala Gln Lys Thr Ser Asp Ile Gln Ser Tyr Leu
130          135          140

Asn Asp Tyr Lys Ser Ala Val Ser Lys Ile Asn Asn Pro Asn Val Ile
145          150          155          160

Asp Ser Asp Phe Glu Ser Leu His Ala Thr Ile Asn Leu Thr Leu Ser
165          170          175

Lys Ile Lys Gly Ser Leu Ser Tyr Phe Ser Ile Phe Asn Gln Pro Asp
180          185          190

Asp Arg Lys Pro Ile Tyr Thr Ile Leu Gly Leu Pro Tyr Tyr Thr Leu
195          200          205

Met Ala Thr Met Tyr Leu Thr Leu Leu Arg Asp Val Ile Leu Asn Thr
210          215          220

Thr Lys Trp Lys Ile Ser Pro Ala Ser Asn Ile Ser Tyr Arg Gln Gln
225          230          235          240

Phe Lys Gln Asn Met Asn Ser Phe Val Leu Thr Ile Lys Asn Asn Tyr
245          250          255

Gln Thr Gly Phe Asn Tyr Ile Thr Asn Glu Ala Tyr Lys Ala His Pro
260          265          270

Thr Asn Pro Ser Lys Thr Ile Leu Pro Phe Glu Asn Lys Met Thr Leu
275          280          285

Asp Cys Phe Asp Tyr Val Ala Met Trp Pro Thr Leu Tyr Pro Asp Asp
290          295          300

Tyr Tyr Thr Glu Lys Thr Asn Leu Gln Lys Thr Arg Leu Leu Phe Ser
305          310          315          320

Pro Ile Leu Gly Arg Met Pro Asp Ser Arg Ser Gln Trp Leu His Ser
325          330          335

Lys Pro Tyr Ser Trp Asp Ser Asn Lys Thr Phe Thr Phe Asp His Tyr
340          345          350

Tyr Met Ala Glu Leu Thr His Ile Asp Thr Lys Glu Phe Asp Arg Val
355          360          365

Asp Arg Ile Arg Gln Ile Tyr Gln Glu Gly Tyr Gln Lys Glu Gln Gln

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Gly	Asn	Tyr	Val	Gly	Thr	Ala	Ile	Lys	Trp	Phe	Asp	Asp	Thr	Gln
			420					425					430	
Gly	Gly	Arg	Ser	Ser	Gly	Tyr	Thr	Thr	Pro	Tyr	Ser	Gly	Asp	Pro
		435					440					445		Asp
Pro	Ile	Ile	Thr	Pro	Asp	Asp	His	Lys	Val	Asn	Phe	Leu	Tyr	Thr
	450					455					460			Val
Lys	Asp	Glu	Leu	Lys	Gly	Ile	Asp	Ala	Trp	Val	Asn	Ser	Trp	Val
465					470					475				480
Ile	Tyr	Thr	Thr	Val	Pro	Asn	Ile	Ile	Glu	Asn	Glu	Met	Phe	Leu
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Thr	Leu	Gly	Phe	Pro	Phe	Glu	Lys	Gly	Ile	Ile	Asp	Thr	Gly	Gly
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Gly	Gly	Asp	Lys	Ile	Tyr	Gln	Leu	Glu	Arg	Leu	Asn	Gly	Ser	Met
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	530					535					540			Leu
Thr	Thr	Gly	Asn	Tyr	Leu	Ile	Arg	Leu	Arg	Tyr	Ala	Ser	His	Ser
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Ile	Asn	Ala	Phe	Thr	His	Ile	His	Ser	Glu	Asn	Gly	Ala	Asp	Ile
				565					570					575
Ser	Thr	Pro	Leu	Gly	Asn	Ile	Thr	Leu	Pro	Asn	Thr	Gln	Asn	Phe
			580					585					590	Thr
Phe	Pro	Thr	Asn	Asp	Glu	Tyr	Gln	Pro	Asn	Gln	Pro	Gln	Tyr	Thr
		595					600					605		Thr
Tyr	Ile	Glu	Gly	Asn	Ala	Gly	Lys	Tyr	Ala	Leu	Tyr	Gln	Phe	Thr
	610					615					620			Gln
Asn	Ile	Ser	Leu	Thr	Ser	Gly	Gln	Tyr	Thr	Phe	Tyr	Ile	Gln	Asn
625					630					635				640
Ser	Asn	Thr	Asp	Leu	Phe	Leu	Asp	Arg	Ile	Glu	Phe	Val	Pro	Met
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Pro	Ser	Ser	Ile	Ser	Leu	Pro	Asp	Ile	Glu	Ile	Thr	Asn	Thr	Asp
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Glu	Ile	Trp	Lys	Ser	Asp	Arg	Pro	Tyr	Gly	His	Ser	Ile	Asn	Gly
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Phe	Ile	Val	Ser	Val	Pro	Phe	Gly	Asn	Gln	Thr	Asp	Thr	Val	Thr
	690					695					700			Ile
Thr	Tyr	Trp	Asn	Asn	Gly	Glu	Lys	Val	His	Thr	Asp	Ser	Gln	Thr
705					710					715				720
Asp	Met	Ala	Arg	Phe	Gln	Gly	Gln	Asp	Leu	Thr	Gln	Trp	Gln	Gly
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Phe	Asp	Arg	Val	Thr	Ile	Arg	Arg	Thr	His	Ser	Asp	Gly	Thr	Leu
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Leu	Thr	Ser	Ala	Thr	Leu	Tyr	Phe	Val	Ile	Pro	Lys	Ser	Ser	Phe
		755					760					765		Ser
Thr	Pro	Glu	Asp	Leu	Glu	Lys	Ile	Thr	Asn	Gln	Val	Asn	Gln	Leu
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Thr	Ser	Ser	Ser	Gln	Thr	Glu	Leu	Ala	Asn	Thr	Val	Thr	Asp	Tyr	Gly
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Ile	Asp	Gln	Val	Leu	Met	Lys	Val	Asp	Ala	Leu	Ser	Asp	Asp	Val	Phe
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Gly	Val	Glu	Lys	Lys	Ala	Leu	Arg	Lys	Leu	Val	Asn	Gln	Ala	Lys	Gln
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Leu	Ser	Lys	Ala	Arg	Asn	Val	Leu	Val	Gly	Gly	Asn	Phe	Glu	Gly	Asn
		835				840						845			
His	Glu	Trp	Val	Leu	Gly	Arg	Lys	Ala	Val	Met	Val	Ala	Asn	Asp	Glu
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Leu	Phe	Lys	Gly	Asn	His	Leu	Leu	Leu	Pro	Pro	Ser	Leu	Tyr	Pro	
865					870					875				880	
Ser	Tyr	Ala	Tyr	Gln	Lys	Val	Asp	Glu	Ser	Lys	Leu	Lys	Pro	Asn	Thr
				885					890					895	
Arg	Tyr	Thr	Val	Ser	Gly	Phe	Val	Ala	Gln	Ser	Glu	Gln	Leu	Glu	Val
			900					905					910		
Val	Val	Ser	Arg	Tyr	Gly	Lys	Glu	Val	His	Asp	Met	Leu	Asn	Val	Pro
		915					920					925			
Tyr	Glu	Glu	Ala	Leu	Pro	Ile	Ser	Ser	Asn	Glu	Lys	Ser	Asn	Cys	Cys
	930					935					940				
Lys	Pro	Ala	Thr	Cys	Asn	Tyr	Thr	Ser	Cys	Glu	Gly	Lys	Glu	Pro	Asp
945					950					955					960
Ser	His	Phe	Phe	Arg	Tyr	Ser	Ile	Asp	Val	Gly	Ala	Leu	Gln	Pro	Glu
				965					970					975	
Ala	Asn	Leu	Gly	Ile	Glu	Phe	Gly	Leu	Arg	Ile	Val	Lys	Ser	Asn	Gly
			980					985					990		
Phe	Ala	Lys	Ile	Ser	Asn	Leu	Glu	Ile	Lys	Glu	Asp	Arg	Pro	Leu	Thr
		995				1000						1005			
Asp	Gln	Glu	Ile	Lys	Lys	Val	Gln	His	Lys	Glu	Gln	Lys	Trp	Lys	Lys
	1010					1015					1020				
Ala	Phe	Asn	Lys	Glu	Gln	Ala	Glu	Leu	Thr	Ala	Thr	Leu	Gln	Pro	Thr
1025					1030					1035				1040	
Leu	Asn	Gln	Ile	Asn	Ala	Leu	Tyr	Gln	Gln	Glu	Asp	Trp	Asn	Gly	Ser
				1045					1050					1055	
Ile	His	Pro	His	Val	Thr	Tyr	Gln	His	Leu	Ser	Asp	Val	Val	Leu	Pro
			1060					1065					1070		
Thr	Leu	Pro	Lys	Gln	Thr	His	Trp	Phe	Met	Glu	Asn	Arg	Glu	Gly	Glu
		1075					1080					1085			
His	Val	Val	Leu	Thr	Gln	Gln	Phe	Gln	Gln	Ala	Leu	Asp	Arg	Ala	Phe
	1090					1095					1100				
Gln	Gln	Ile	Glu	Glu	Gln	Asn	Leu	Ile	His	Asn	Gly	Ser	Phe	Thr	Ser
1105					1110					1115				1120	
Gly	Leu	Thr	Asp	Trp	Thr	Val	Thr	Gly	Asp	Ala	Gln	Ile	Thr	Ile	Tyr
				1125					1130					1135	
Asp	Glu	Asp	Pro	Val	Leu	Glu	Leu	Ala	His	Trp	Asp	Ala	Ser	Val	Ser
			1140					1145					1150		
Gln	Thr	Ile	Glu	Ile	Thr	Asp	Phe	Glu	Glu	Glu	Lys	Glu	Tyr	Lys	Leu
	1155						1160					1165			
Arg	Val	Arg	Gly	Lys	Gly	Lys	Gly	Thr	Val	Thr	Val	Gln	His	Glu	Glu
	1170					1175						1180			

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Glu Leu Glu Thr Met Thr Phe Asn Thr Thr Ser Phe Thr Thr Lys Glu
 1185 1190 1195 1200

Gln Thr Phe Tyr Phe Glu Gly Asn Thr Ile Asp Val His Val Gln Ser
 1205 1210 1215

Glu Asn Asn Ala Phe Leu Val Asp Ser Val Glu Leu Ile Glu Val Val
 1220 1225 1230

Lys Glu Gln Glu Glu Lys Gln
 1235

<210> SEQ ID NO 7
 <211> LENGTH: 2059
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synaxmi-031
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(2058)

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1 5 10 15	
gct atc cct gtt agc aat gtt aat agc ctt acg gat acg gtt ggc gat	96
Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp	
20 25 30	
cta aag aag gca tgg gaa gag ttc cag aag acg ggc agc ttc tcc ctt	144
Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu	
35 40 45	
acc gca ctc cag cag ggc ttc agc gct tcc cag ggc ggg acg ttc aat	192
Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn	
50 55 60	
tac ctc acc ctc ctc cag tcc ggg atc tcc ctg gct ggc agc ttc gtg	240
Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val	
65 70 75 80	
cct ggc ggc acc ttc gtt gct cca atc atc aat atg gtg atc ggc tgg	288
Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp	
85 90 95	
ctc tgg cct cat aag aat aag aat gca gat acg gaa aat ctg atc aat	336
Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn	
100 105 110	
ctg atc gat tca gaa atc cag aag cag ctg aat aag gct ctg ctg gat	384
Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp	
115 120 125	
gct gat cgc aat gaa tgg agc agc tac ctc gag tcc atc ttc gat agc	432
Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser	
130 135 140	
agc aat aat ctg aat ggc gca atc gtt gat gct cag tgg tcc ggc acc	480
Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr	
145 150 155 160	
gtg aat acg acc aat cgt acg ctt cgt aat cct acg gaa tca gat tac	528
Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr	
165 170 175	
acc aat gtg gtg acg aat ttc atc gca gca gat ggg gat atc gct aat	576
Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn	
180 185 190	
aat gaa aat cat atc atg aat ggg aat ttc gat gtg gca gca gct cca	624
Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Pro	
195 200 205	

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tac ttc gtt atc ggg gct acc gct aga ttc gca gct atg cag tcc tac	672
Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr	
210 215 220	
atc aag ttc tgc aat gca tgg atc gat aag gtt ggg ctg tca gat gct	720
Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala	
225 230 235 240	
cag ctg acc acg cag aag gct aat ctg gat aga acg aag cag aat atg	768
Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met	
245 250 255	
cgt aat gct atc ctt aat tac acc cag cag gtt atg aag gtt ttc aag	816
Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys	
260 265 270	
gat tcc aag aat atg cca acg atc ggc acg aat aag ttc agc gtt gat	864
Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp	
275 280 285	
acc tac aat gtt tac atc aag ggg atg acg ctt aat gtg ctt gat atc	912
Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile	
290 295 300	
gtt gct atc tgg cca agc ctg tac cca gat gat tac acg tca cag acg	960
Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr	
305 310 315 320	
gct ctg gaa cag acc cgc gtg acg ttc tcc aat atg gtg ggg cag gaa	1008
Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu	
325 330 335	
gaa ggc acg gat ggc agc ctc aga atc tac aat acc ttc gat agc ttc	1056
Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe	
340 345 350	
tcc tac cag cat agc cct atc cct aat aat aat gtg aat ctc atc agc	1104
Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser	
355 360 365	
tac tac aat gat gaa ctt cag aat ctg gaa ctc ggg gtt tac acc cca	1152
Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro	
370 375 380	
cca aag aag ggc tca ggc tac agc tac cca tac ggg ttc gtg ctg aat	1200
Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn	
385 390 395 400	
tac gca aat agc aag tac aag tac ggc gat tcc aat gat cca gaa tcc	1248
Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser	
405 410 415	
ctc ggc ggg ctt tcc acc ctt agc gct cca atc caa cag gtt aat gct	1296
Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala	
420 425 430	
gct acc cag aat agc aag tac ctt gat ggc gaa atc ctg aat ggg atc	1344
Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile	
435 440 445	
ggc gca agc ctg cct ggc tac tgc acg acc ggg tgc tca cct acc gaa	1392
Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu	
450 455 460	
cca cca ttc agc tgc acg agc acg gca aat ggg tac aag gca agc tgc	1440
Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys	
465 470 475 480	
aat cca agc gat acc aat cag aag atc aat gct ctc tac cca ttc acg	1488
Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr	
485 490 495	
cag gca aat gtg aag ggg aat acc ggg aag ctg ggc gtt ctc gca agc	1536
Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser	
500 505 510	

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ctt gtt agc tac gat ctg aat cct aag aat gtt ttc ggg gaa ctc gat Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp 515 520 525	1584
tca gat acc aat aat gtt atc ctt aag ggc atc cca gca gaa aag ggc Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly 530 535 540	1632
tac ttc cca aat aat gca aga cca acc gtt gtg aag gaa tgg atc aat Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn 545 550 555 560	1680
ggg gct tcc gca gtt cca ctt gat tcc ggc aat acc ctg ttc atg acg Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr 565 570 575	1728
gct acg aac ctg acg gct acc cag tac aga atc cgc atc cgt tac gct Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala 580 585 590	1776
aac cca aac tca aac acg cag atc ggc gtt aga atc acg cag aac ggg Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly 595 600 605	1824
agc ctc atc tcc tcc tcc aac ctc acg ctg tac tca acc acc gat atg Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met 610 615 620	1872
aac aac acc ctg cca ctg aac gtt tac gtg atc ggg gaa aac ggg aac Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn 625 630 635 640	1920
tac acc ctc cag gat ctc tac aac acg acg aac gtt ctg tcc acg ggc Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly 645 650 655	1968
gat atc acc ctg cag atc acc ggc ggg gat cag aag ata ttc atc gat Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp 660 665 670	2016
cgc atc gag ttc gtg cct acg atg cca gtg cca ggc aac taa Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn * 675 680 685	2058
a	2059

<210> SEQ ID NO 8
 <211> LENGTH: 685
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: SYNAXMI-031

<400> SEQUENCE: 8

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Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp 20 25 30
Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu 35 40 45
Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn 50 55 60
Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val 65 70 75 80
Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp 85 90 95
Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn

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100						105						110					
Leu	Ile	Asp	Ser	Glu	Ile	Gln	Lys	Gln	Leu	Asn	Lys	Ala	Leu	Leu	Asp		
115						120						125					
Ala	Asp	Arg	Asn	Glu	Trp	Ser	Ser	Tyr	Leu	Glu	Ser	Ile	Phe	Asp	Ser		
130						135						140					
Ser	Asn	Asn	Leu	Asn	Gly	Ala	Ile	Val	Asp	Ala	Gln	Trp	Ser	Gly	Thr		
145						150						155					
Val	Asn	Thr	Thr	Asn	Arg	Thr	Leu	Arg	Asn	Pro	Thr	Glu	Ser	Asp	Tyr		
165						170						175					
Thr	Asn	Val	Val	Thr	Asn	Phe	Ile	Ala	Ala	Asp	Gly	Asp	Ile	Ala	Asn		
180						185						190					
Asn	Glu	Asn	His	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala	Ala	Ala	Pro		
195						200						205					
Tyr	Phe	Val	Ile	Gly	Ala	Thr	Ala	Arg	Phe	Ala	Ala	Met	Gln	Ser	Tyr		
210						215						220					
Ile	Lys	Phe	Cys	Asn	Ala	Trp	Ile	Asp	Lys	Val	Gly	Leu	Ser	Asp	Ala		
225						230						235					
Gln	Leu	Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys	Gln	Asn	Met		
245						250						255					
Arg	Asn	Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys	Val	Phe	Lys		
260						265						270					
Asp	Ser	Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val	Asp		
275						280						285					
Thr	Tyr	Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	Ile		
290						295						300					
Val	Ala	Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr	Ser	Gln	Thr		
305						310						315					
Ala	Leu	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	Glu		
325						330						335					
Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Phe		
340						345						350					
Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser		
355						360						365					
Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	Pro		
370						375						380					
Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn		
385						390						395					
Tyr	Ala	Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu	Ser		
405						410						415					
Leu	Gly	Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn	Ala		
420						425						430					
Ala	Thr	Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu	Asn	Gly	Ile		
435						440						445					
Gly	Ala	Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr	Glu		
450						455						460					
Pro	Pro	Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser	Cys		
465						470						475					
Asn	Pro	Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe	Thr		
485						490						495					
Gln	Ala	Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	Ser		
500						505						510					

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Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp
 515 520 525
 Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly
 530 535 540
 Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn
 545 550 555 560
 Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr
 565 570 575
 Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala
 580 585 590
 Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly
 595 600 605
 Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met
 610 615 620
 Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn
 625 630 635 640
 Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly
 645 650 655
 Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp
 660 665 670
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 675 680 685

<210> SEQ ID NO 9
 <211> LENGTH: 2148
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synaxmi-031(apo)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(2148)

<400> SEQUENCE: 9

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gtt gtt tgc aat ggg ggc aag acg tcc acc tac gtg cgt aat ctg gat	96
Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg Asn Leu Asp	
20 25 30	
tgc aat ctc cag agc cag cag aat atc cca tac aat gtg ctt gct atc	144
Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu Ala Ile	
35 40 45	
cct gtt agc aat gtt aat agc ctt acg gat acg gtt ggc gat cta aag	192
Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp Leu Lys	
50 55 60	
aag gca tgg gaa gag ttc cag aag acg ggc agc ttc tcc ctt acc gca	240
Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu Thr Ala	
65 70 75 80	
ctc cag cag ggc ttc agc gct tcc cag ggc ggg acg ttc aat tac ctc	288
Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn Tyr Leu	
85 90 95	
acc ctc ctc cag tcc ggg atc tcc ctg gct ggc agc ttc gtg cct ggc	336
Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val Pro Gly	
100 105 110	
ggc acc ttc gtt gct cca atc atc aat atg gtg atc ggc tgg ctc tgg	384

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Gly	Thr	Phe	Val	Ala	Pro	Ile	Ile	Asn	Met	Val	Ile	Gly	Trp	Leu	Trp	
	115						120					125				
cct	cat	aag	aat	aag	aat	gca	gat	acg	gaa	aat	ctg	atc	aat	ctg	atc	432
Pro	His	Lys	Asn	Lys	Asn	Ala	Asp	Thr	Glu	Asn	Leu	Ile	Asn	Leu	Ile	
	130						135				140					
gat	tca	gaa	atc	cag	aag	cag	ctg	aat	aag	gct	ctg	ctg	gat	gct	gat	480
Asp	Ser	Glu	Ile	Gln	Lys	Gln	Leu	Asn	Lys	Ala	Leu	Leu	Asp	Ala	Asp	
	145					150				155					160	
cgc	aat	gaa	tgg	agc	agc	tac	ctc	gag	tcc	atc	ttc	gat	agc	agc	aat	528
Arg	Asn	Glu	Trp	Ser	Ser	Tyr	Leu	Glu	Ser	Ile	Phe	Asp	Ser	Ser	Asn	
				165					170						175	
aat	ctg	aat	ggc	gca	atc	gtt	gat	gct	cag	tgg	tcc	ggc	acc	gtg	aat	576
Asn	Leu	Asn	Gly	Ala	Ile	Val	Asp	Ala	Gln	Trp	Ser	Gly	Thr	Val	Asn	
			180					185						190		
acg	acc	aat	cgt	acg	ctt	cgt	aat	cct	acg	gaa	tca	gat	tac	acc	aat	624
Thr	Thr	Asn	Arg	Thr	Leu	Arg	Asn	Pro	Thr	Glu	Ser	Asp	Tyr	Thr	Asn	
		195					200					205				
gtg	gtg	acg	aat	ttc	atc	gca	gca	gat	ggg	gat	atc	gct	aat	aat	gaa	672
Val	Val	Thr	Asn	Phe	Ile	Ala	Ala	Asp	Gly	Asp	Ile	Ala	Asn	Asn	Glu	
	210					215					220					
aat	cat	atc	atg	aat	ggg	aat	ttc	gat	gtg	gca	gca	gct	cca	tac	ttc	720
Asn	His	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala	Ala	Ala	Pro	Tyr	Phe	
	225				230					235					240	
gtt	atc	ggg	gct	acc	gct	aga	ttc	gca	gct	atg	cag	tcc	tac	atc	aag	768
Val	Ile	Gly	Ala	Thr	Ala	Arg	Phe	Ala	Ala	Met	Gln	Ser	Tyr	Ile	Lys	
				245					250					255		
ttc	tgc	aat	gca	tgg	atc	gat	aag	gtt	ggg	ctg	tca	gat	gct	cag	ctg	816
Phe	Cys	Asn	Ala	Trp	Ile	Asp	Lys	Val	Gly	Leu	Ser	Asp	Ala	Gln	Leu	
			260				265						270			
acc	acg	cag	aag	gct	aat	ctg	gat	aga	acg	aag	cag	aat	atg	cgt	aat	864
Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys	Gln	Asn	Met	Arg	Asn	
		275				280						285				
gct	atc	ctt	aat	tac	acc	cag	cag	gtt	atg	aag	gtt	ttc	aag	gat	tcc	912
Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys	Val	Phe	Lys	Asp	Ser	
	290					295					300					
aag	aat	atg	cca	acg	atc	ggc	acg	aat	aag	ttc	agc	gtt	gat	acc	tac	960
Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val	Asp	Thr	Tyr	
	305				310				315					320		
aat	gtt	tac	atc	aag	ggg	atg	acg	ctt	aat	gtg	ctt	gat	atc	gtt	gct	1008
Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	Ile	Val	Ala	
			325						330					335		
atc	tgg	cca	agc	ctg	tac	cca	gat	gat	tac	acg	tca	cag	acg	gct	ctg	1056
Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr	Ser	Gln	Thr	Ala	Leu	
			340					345					350			
gaa	cag	acc	cgc	gtg	acg	ttc	tcc	aat	atg	gtg	ggg	cag	gaa	gaa	ggc	1104
Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	Glu	Glu	Gly	
		355					360					365				
acg	gat	ggc	agc	ctc	aga	atc	tac	aat	acc	ttc	gat	agc	ttc	tcc	tac	1152
Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Phe	Ser	Tyr	
	370				375					380						
cag	cat	agc	cct	atc	cct	aat	aat	aat	gtg	aat	ctc	atc	agc	tac	tac	1200
Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser	Tyr	Tyr	
	385				390					395					400	
aat	gat	gaa	ctt	cag	aat	ctg	gaa	ctc	ggg	gtt	tac	acc	cca	cca	aag	1248
Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	Pro	Pro	Lys	
				405				410					415			
aag	ggc	tca	ggc	tac	agc	tac	cca	tac	ggg	ttc	gtg	ctg	aat	tac	gca	1296

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Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn	Tyr	Ala	
			420					425					430			
aat	agc	aag	tac	aag	tac	ggc	gat	tcc	aat	gat	cca	gaa	tcc	ctc	ggc	1344
Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu	Ser	Leu	Gly	
		435					440					445				
ggg	ctt	tcc	acc	ctt	agc	gct	cca	atc	caa	cag	gtt	aat	gct	gct	acc	1392
Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn	Ala	Ala	Thr	
	450					455					460					
cag	aat	agc	aag	tac	ctt	gat	ggc	gaa	atc	ctg	aat	ggg	atc	ggc	gca	1440
Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu	Asn	Gly	Ile	Gly	Ala	
465					470					475					480	
agc	ctg	cct	ggc	tac	tgc	acg	acc	ggg	tgc	tca	cct	acc	gaa	cca	cca	1488
Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr	Glu	Pro	Pro	
				485					490					495		
ttc	agc	tgc	acg	agc	acg	gca	aat	ggg	tac	aag	gca	agc	tgc	aat	cca	1536
Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser	Cys	Asn	Pro	
			500					505						510		
agc	gat	acc	aat	cag	aag	atc	aat	gct	ctc	tac	cca	ttc	acg	cag	gca	1584
Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe	Thr	Gln	Ala	
		515					520					525				
aat	gtg	aag	ggg	aat	acc	ggg	aag	ctg	ggc	gtt	ctc	gca	agc	ctt	gtt	1632
Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	Ser	Leu	Val	
	530						535				540					
agc	tac	gat	ctg	aat	cct	aag	aat	gtt	ttc	ggg	gaa	ctc	gat	tca	gat	1680
Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu	Asp	Ser	Asp	
	545				550					555					560	
acc	aat	aat	gtt	atc	ctt	aag	ggc	atc	cca	gca	gaa	aag	ggc	tac	ttc	1728
Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys	Gly	Tyr	Phe	
				565				570						575		
cca	aat	aat	gca	aga	cca	acc	gtt	gtg	aag	gaa	tgg	atc	aat	ggg	gct	1776
Pro	Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu	Trp	Ile	Asn	Gly	Ala	
			580					585					590			
tcc	gca	gtt	cca	ctt	gat	tcc	ggc	aat	acc	ctg	ttc	atg	acg	gct	acg	1824
Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met	Thr	Ala	Thr	
		595					600					605				
aac	ctg	acg	gct	acc	cag	tac	aga	atc	cgc	atc	cgt	tac	gct	aac	cca	1872
Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr	Ala	Asn	Pro	
	610					615					620					
aac	tca	aac	acg	cag	atc	ggc	gtt	aga	atc	acg	cag	aac	ggg	agc	ctc	1920
Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn	Gly	Ser	Leu	
	625				630					635					640	
atc	tcc	tcc	tcc	aac	ctc	acg	ctg	tac	tca	acc	acc	gat	atg	aac	aac	1968
Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp	Met	Asn	Asn	
				645					650					655		
acc	ctg	cca	ctg	aac	gtt	tac	gtg	atc	ggg	gaa	aac	ggg	aac	tac	acc	2016
Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly	Asn	Tyr	Thr	
			660				665						670			
ctc	cag	gat	ctc	tac	aac	acg	acg	aac	gtt	ctg	tcc	acg	ggc	gat	atc	2064
Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr	Gly	Asp	Ile	
		675					680					685				
acc	ctg	cag	atc	acc	ggc	ggg	gat	cag	aag	ata	ttc	atc	gat	cgc	atc	2112
Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile	Asp	Arg	Ile	
		690				695					700					
gag	ttc	gtg	cct	acg	atg	cca	gtg	cca	ggc	aac	taa					2148
Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn	*					
705					710					715						

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<210> SEQ ID NO 10
<211> LENGTH: 715
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: SYNAXMI-031(APO)

<400> SEQUENCE: 10

Met Gly Tyr Ser Ser Phe Val Ala Ile Ala Leu Leu Met Ser Val Val
 1             5             10             15

Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg Asn Leu Asp
 20             25             30

Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu Ala Ile
 35             40             45

Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp Leu Lys
 50             55             60

Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu Thr Ala
 65             70             75             80

Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn Tyr Leu
 85             90             95

Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val Pro Gly
 100            105            110

Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp Leu Trp
 115            120            125

Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn Leu Ile
 130            135            140

Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp Ala Asp
 145            150            155            160

Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser Ser Asn
 165            170            175

Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr Val Asn
 180            185            190

Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr Thr Asn
 195            200            205

Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn Asn Glu
 210            215            220

Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro Tyr Phe
 225            230            235            240

Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr Ile Lys
 245            250            255

Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala Gln Leu
 260            265            270

Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met Arg Asn
 275            280            285

Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys Asp Ser
 290            295            300

Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp Thr Tyr
 305            310            315            320

Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile Val Ala
 325            330            335

Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr Ala Leu
 340            345            350

Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu Glu Gly

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355	360	365
Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe Ser Tyr 370 375 380		
Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser Tyr Tyr 385 390 395 400		
Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro Pro Lys 405 410 415		
Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn Tyr Ala 420 425 430		
Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser Leu Gly 435 440 445		
Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala Ala Thr 450 455 460		
Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile Gly Ala 465 470 475 480		
Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu Pro Pro 485 490 495		
Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys Asn Pro 500 505 510		
Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr Gln Ala 515 520 525		
Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser Leu Val 530 535 540		
Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp Ser Asp 545 550 555 560		
Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly Tyr Phe 565 570 575		
Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn Gly Ala 580 585 590		
Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr Ala Thr 595 600 605		
Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala Asn Pro 610 615 620		
Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly Ser Leu 625 630 635 640		
Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met Asn Asn 645 650 655		
Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn Tyr Thr 660 665 670		
Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly Asp Ile 675 680 685		
Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp Arg Ile 690 695 700		
Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn 705 710 715		

<210> SEQ ID NO 11

<211> LENGTH: 2160

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synaxmi-031(ER)

<220> FEATURE:

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<221> NAME/KEY: CDS

<222> LOCATION: (1)...(2160)

<400> SEQUENCE: 11

atg ggg tac tcc agc ttc gtt gct atc gct ctt ctt atg agc gtg gtt	48
Met Gly Tyr Ser Ser Phe Val Ala Ile Ala Leu Leu Met Ser Val Val	
1 5 10 15	
gtt gtt tgc aat ggg ggc aag acg tcc acc tac gtg cgt aat ctg gat	96
Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg Asn Leu Asp	
20 25 30	
tgc aat ctc cag agc cag cag aat atc cca tac aat gtg ctt gct atc	144
Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu Ala Ile	
35 40 45	
cct gtt agc aat gtt aat agc ctt acg gat acg gtt ggc gat cta aag	192
Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp Leu Lys	
50 55 60	
aag gca tgg gaa gag ttc cag aag acg ggc agc ttc tcc ctt acc gca	240
Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu Thr Ala	
65 70 75 80	
ctc cag cag ggc ttc agc gct tcc cag ggc ggg acg ttc aat tac ctc	288
Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn Tyr Leu	
85 90 95	
acc ctc ctc cag tcc ggg atc tcc ctg gct ggc agc ttc gtg cct ggc	336
Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val Pro Gly	
100 105 110	
ggc acc ttc gtt gct cca atc atc aat atg gtg atc ggc tgg ctc tgg	384
Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp Leu Trp	
115 120 125	
cct cat aag aat aag aat gca gat acg gaa aat ctg atc aat ctg atc	432
Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn Leu Ile	
130 135 140	
gat tca gaa atc cag aag cag ctg aat aag gct ctg ctg gat gct gat	480
Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp Ala Asp	
145 150 155 160	
cgc aat gaa tgg agc agc tac ctc gag tcc atc ttc gat agc agc aat	528
Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser Ser Asn	
165 170 175	
aat ctg aat ggc gca atc gtt gat gct cag tgg tcc ggc acc gtg aat	576
Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr Val Asn	
180 185 190	
acg acc aat cgt acg ctt cgt aat cct acg gaa tca gat tac acc aat	624
Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr Thr Asn	
195 200 205	
gtg gtg acg aat ttc atc gca gca gat ggg gat atc gct aat aat gaa	672
Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn Asn Glu	
210 215 220	
aat cat atc atg aat ggg aat ttc gat gtg gca gca gct cca tac ttc	720
Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Pro Tyr Phe	
225 230 235 240	
gtt atc ggg gct acc gct aga ttc gca gct atg cag tcc tac atc aag	768
Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr Ile Lys	
245 250 255	
ttc tgc aat gca tgg atc gat aag gtt ggg ctg tca gat gct cag ctg	816
Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala Gln Leu	
260 265 270	
acc acg cag aag gct aat ctg gat aga acg aag cag aat atg cgt aat	864
Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met Arg Asn	
275 280 285	

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gct atc ctt aat tac acc cag cag gtt atg aag gtt ttc aag gat tcc	912
Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys Asp Ser	
290 295 300	
aag aat atg cca acg atc ggc acg aat aag ttc agc gtt gat acc tac	960
Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp Thr Tyr	
305 310 315 320	
aat gtt tac atc aag ggg atg acg ctt aat gtg ctt gat atc gtt gct	1008
Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile Val Ala	
325 330 335	
atc tgg cca agc ctg tac cca gat gat tac acg tca cag acg gct ctg	1056
Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr Ala Leu	
340 345 350	
gaa cag acc cgc gtg acg ttc tcc aat atg gtg ggg cag gaa gaa ggc	1104
Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu Glu Gly	
355 360 365	
acg gat ggc agc ctc aga atc tac aat acc ttc gat agc ttc tcc tac	1152
Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe Ser Tyr	
370 375 380	
cag cat agc cct atc cct aat aat aat gtg aat ctc atc agc tac tac	1200
Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser Tyr Tyr	
385 390 395 400	
aat gat gaa ctt cag aat ctg gaa ctc ggg gtt tac acc cca cca aag	1248
Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro Pro Lys	
405 410 415	
aag ggc tca ggc tac agc tac cca tac ggg ttc gtg ctg aat tac gca	1296
Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn Tyr Ala	
420 425 430	
aat agc aag tac aag tac ggc gat tcc aat gat cca gaa tcc ctc ggc	1344
Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser Leu Gly	
435 440 445	
ggg ctt tcc acc ctt agc gct cca atc caa cag gtt aat gct gct acc	1392
Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala Ala Thr	
450 455 460	
cag aat agc aag tac ctt gat ggc gaa atc ctg aat ggg atc ggc gca	1440
Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile Gly Ala	
465 470 475 480	
agc ctg cct ggc tac tgc acg acc ggg tgc tca cct acc gaa cca cca	1488
Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu Pro Pro	
485 490 495	
ttc agc tgc acg agc acg gca aat ggg tac aag gca agc tgc aat cca	1536
Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys Asn Pro	
500 505 510	
agc gat acc aat cag aag atc aat gct ctc tac cca ttc acg cag gca	1584
Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr Gln Ala	
515 520 525	
aat gtg aag ggg aat acc ggg aag ctg ggc gtt ctc gca agc ctt gtt	1632
Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser Leu Val	
530 535 540	
agc tac gat ctg aat cct aag aat gtt ttc ggg gaa ctc gat tca gat	1680
Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp Ser Asp	
545 550 555 560	
acc aat aat gtt atc ctt aag ggc atc cca gca gaa aag ggc tac ttc	1728
Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly Tyr Phe	
565 570 575	
cca aat aat gca aga cca acc gtt gtg aag gaa tgg atc aat ggg gct	1776
Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn Gly Ala	
580 585 590	

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tcc gca gtt cca ctt gat tcc ggc aat acc ctg ttc atg acg gct acg	1824
Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr Ala Thr	
595 600 605	
aac ctg acg gct acc cag tac aga atc cgc atc cgt tac gct aac cca	1872
Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala Asn Pro	
610 615 620	
aac tca aac acg cag atc ggc gtt aga atc acg cag aac ggg agc ctc	1920
Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly Ser Leu	
625 630 635 640	
atc tcc tcc tcc aac ctc acg ctg tac tca acc acc gat atg aac aac	1968
Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met Asn Asn	
645 650 655	
acc ctg cca ctg aac gtt tac gtg atc ggg gaa aac ggg aac tac acc	2016
Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn Tyr Thr	
660 665 670	
ctc cag gat ctc tac aac acg acg aac gtt ctg tcc acg ggc gat atc	2064
Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly Asp Ile	
675 680 685	
acc ctg cag atc acc ggc ggg gat cag aag ata ttc atc gat cgc atc	2112
Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp Arg Ile	
690 695 700	
gag ttc gtg cct acg atg cca gtg cca ggc aac aag gat gaa ctg taa	2160
Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Lys Asp Glu Leu *	
705 710 715	

<210> SEQ ID NO 12

<211> LENGTH: 719

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: SYNAXMI-031(ER)

<400> SEQUENCE: 12

Met Gly Tyr Ser Ser Phe Val Ala Ile Ala Leu Leu Met Ser Val Val	
1 5 10 15	
Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg Asn Leu Asp	
20 25 30	
Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu Ala Ile	
35 40 45	
Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp Leu Lys	
50 55 60	
Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu Thr Ala	
65 70 75 80	
Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn Tyr Leu	
85 90 95	
Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val Pro Gly	
100 105 110	
Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp Leu Trp	
115 120 125	
Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn Leu Ile	
130 135 140	
Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp Ala Asp	
145 150 155 160	
Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser Ser Asn	
165 170 175	

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Asn	Leu	Asn	Gly	Ala	Ile	Val	Asp	Ala	Gln	Trp	Ser	Gly	Thr	Val	Asn
			180					185					190		
Thr	Thr	Asn	Arg	Thr	Leu	Arg	Asn	Pro	Thr	Glu	Ser	Asp	Tyr	Thr	Asn
		195					200					205			
Val	Val	Thr	Asn	Phe	Ile	Ala	Ala	Asp	Gly	Asp	Ile	Ala	Asn	Asn	Glu
		210				215					220				
Asn	His	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala	Ala	Ala	Pro	Tyr	Phe
225					230					235					240
Val	Ile	Gly	Ala	Thr	Ala	Arg	Phe	Ala	Ala	Met	Gln	Ser	Tyr	Ile	Lys
				245				250						255	
Phe	Cys	Asn	Ala	Trp	Ile	Asp	Lys	Val	Gly	Leu	Ser	Asp	Ala	Gln	Leu
		260					265						270		
Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys	Gln	Asn	Met	Arg	Asn
		275					280					285			
Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys	Val	Phe	Lys	Asp	Ser
		290				295					300				
Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val	Asp	Thr	Tyr
305					310					315					320
Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	Ile	Val	Ala
				325				330						335	
Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr	Ser	Gln	Thr	Ala	Leu
		340					345						350		
Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	Glu	Glu	Gly
		355				360						365			
Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Phe	Ser	Tyr
	370					375					380				
Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser	Tyr	Tyr
385					390					395					400
Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	Pro	Pro	Lys
			405					410					415		
Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn	Tyr	Ala
		420					425					430			
Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu	Ser	Leu	Gly
		435				440					445				
Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn	Ala	Ala	Thr
	450					455					460				
Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu	Asn	Gly	Ile	Gly	Ala
465					470					475					480
Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr	Glu	Pro	Pro
			485					490					495		
Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser	Cys	Asn	Pro
		500					505					510			
Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe	Thr	Gln	Ala
		515				520						525			
Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	Ser	Leu	Val
	530					535				540					
Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu	Asp	Ser	Asp
545					550				555						560
Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys	Gly	Tyr	Phe
			565					570						575	
Pro	Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu	Trp	Ile	Asn	Gly	Ala

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580					585					590					
Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met	Thr	Ala	Thr
595					600					605					
Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr	Ala	Asn	Pro
610					615					620					
Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn	Gly	Ser	Leu
625					630					635					
Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp	Met	Asn	Asn
645					650					655					
Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly	Asn	Tyr	Thr
660					665					670					
Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr	Gly	Asp	Ile
675					680					685					
Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile	Asp	Arg	Ile
690					695					700					
Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn	Lys	Asp	Glu	Leu	
705					710					715					

<210> SEQ ID NO 13

<211> LENGTH: 1186

<212> TYPE: PRT

<213> ORGANISM: Bacillus thuringiensis

<400> SEQUENCE: 13

Met	Asp	Cys	Asn	Leu	Gln	Ser	Gln	Gln	Asn	Ile	Pro	Tyr	Asn	Val	Leu
1				5					10					15	
Ala	Ile	Pro	Val	Ser	Asn	Val	Asn	Ala	Leu	Val	Asp	Thr	Ala	Gly	Asp
			20					25					30		
Leu	Lys	Lys	Ala	Trp	Glu	Glu	Phe	Gln	Lys	Thr	Gly	Ser	Phe	Ser	Leu
	35						40					45			
Thr	Ala	Leu	Gln	Gln	Gly	Phe	Ser	Ala	Ser	Gln	Gly	Gly	Ala	Phe	Asn
	50					55					60				
Tyr	Leu	Thr	Leu	Leu	Gln	Ser	Gly	Ile	Ser	Leu	Ala	Gly	Ser	Phe	Val
	65				70					75				80	
Pro	Gly	Gly	Thr	Phe	Val	Ala	Pro	Ile	Val	Asn	Met	Val	Ile	Gly	Trp
			85					90						95	
Leu	Trp	Pro	His	Lys	Asn	Lys	Thr	Ala	Asp	Thr	Glu	Asn	Leu	Ile	Lys
		100						105					110		
Leu	Ile	Asp	Glu	Glu	Ile	Gln	Lys	Gln	Leu	Asn	Lys	Ala	Leu	Leu	Asp
		115					120					125			
Gln	Asp	Arg	Asn	Asn	Trp	Thr	Ser	Phe	Leu	Glu	Ser	Ile	Phe	Asp	Thr
	130					135					140				
Ser	Ala	Thr	Val	Ser	Asn	Ala	Ile	Ile	Asp	Ala	Gln	Trp	Ser	Gly	Thr
	145				150					155				160	
Val	Asp	Thr	Thr	Asn	Arg	Gln	Gln	Lys	Thr	Pro	Thr	Thr	Ser	Asp	Tyr
			165					170						175	
Leu	Asn	Val	Val	Gly	Lys	Phe	Asp	Ser	Ala	Asp	Ser	Ser	Ile	Ile	Thr
		180						185					190		
Asn	Glu	Asn	Gln	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala	Ala	Ala	Pro
	195						200					205			
Tyr	Phe	Val	Ile	Gly	Ala	Thr	Leu	Arg	Leu	Ser	Leu	Tyr	Gln	Ser	Tyr
	210					215					220				

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Ile	Lys	Phe	Cys	Asn	Ser	Trp	Ile	Asp	Ala	Val	Gly	Phe	Ser	Thr	Asn	
225					230					235					240	
Asp	Ala	Asn	Thr	Gln	Lys	Ala	Asn	Leu	Ala	Arg	Thr	Lys	Leu	Thr	Met	
				245					250					255		
Arg	Thr	Thr	Ile	Asn	Glu	Tyr	Thr	Gln	Arg	Val	Met	Lys	Val	Phe	Lys	
			260					265					270			
Asp	Ser	Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val	Asp	
		275					280					285				
Ala	Tyr	Asn	Val	Tyr	Val	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	Met	
	290					295					300					
Val	Ala	Ile	Trp	Ser	Ser	Leu	Tyr	Pro	Asn	Asp	Tyr	Thr	Ser	Gln	Thr	
305					310					315					320	
Ala	Ile	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	Glu	
				325					330					335		
Glu	Gly	Thr	Asp	Gly	Thr	Leu	Lys	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Leu	
		340						345					350			
Ser	Tyr	Gln	His	Ser	Leu	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser	
		355					360					365				
Tyr	Tyr	Thr	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Ala	Val	Tyr	Thr	Pro	
	370					375					380					
Lys	Gly	Gly	Ser	Gly	Tyr	Ala	Tyr	Pro	Tyr	Gly	Phe	Ile	Leu	Asn	Tyr	
385					390					395					400	
Ala	Asn	Ser	Asn	Tyr	Lys	Tyr	Gly	Asp	Asn	Asp	Pro	Thr	Gly	Lys	Pro	
				405					410					415		
Leu	Asn	Lys	Gln	Asp	Gly	Pro	Ile	Gln	Gln	Ile	Asn	Ala	Ala	Thr	Gln	
		420						425					430			
Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Thr	Ile	Asn	Gly	Ile	Gly	Ala	Ser	
		435					440					445				
Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Ala	Thr	Glu	Gln	Pro	Phe	
	450					455					460					
Ser	Cys	Thr	Ser	Thr	Ala	Asn	Ser	Tyr	Lys	Ala	Ser	Cys	Asn	Pro	Ser	
465					470					475					480	
Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Ala	Phe	Thr	Gln	Thr	Asn	
			485						490					495		
Val	Lys	Gly	Ser	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	Ser	Leu	Val	Pro	
		500						505					510			
Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu	Asp	Ser	Asp	Thr	
	515						520					525				
Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys	Gly	Tyr	Phe	Pro	
	530					535					540					
Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu	Trp	Ile	Asn	Gly	Ala	Ser	
545					550					555					560	
Ala	Val	Pro	Phe	Tyr	Ser	Gly	Asn	Thr	Leu	Phe	Met	Thr	Ala	Thr	Asn	
			565						570					575		
Leu	Thr	Ala	Thr	Gln	Tyr	Lys	Ile	Arg	Ile	Arg	Tyr	Ala	Asn	Pro	Asn	
		580						585					590			
Ser	Asp	Thr	Gln	Ile	Gly	Val	Leu	Ile	Thr	Gln	Asn	Gly	Ser	Gln	Ile	
		595					600					605				
Ser	Asn	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp	Ser	Ser	Met	Ser	
	610					615					620					
Ser	Asn	Leu	Pro	Gln	Asn	Val	Tyr	Val	Thr	Gly	Glu	Asn	Gly	Asn	Tyr	

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625	630	635	640
Thr Leu Leu Asp 645	Tyr Ser Thr Thr	Asn Val Leu Ser 650	Thr Gly Asp 655
Ile Thr Leu Lys 660	Leu Thr Gly Gly	Asn Gln Lys Ile Phe 665	Ile Asp Arg 670
Ile Glu Phe 675	Ile Pro Thr Met 680	Pro Val Pro Ala Pro 685	Thr Asn Asn Thr
Asn Asn Asn Asn Gly 690	Asp Asn Gly Asn Asn 695	Asn Asn Pro Pro His 700	His Gly
Cys Ala Ile Ala Gly 705	Thr Gln Gln Leu Cys 710	Ser Gly Pro Pro Lys 715	Phe 720
Glu Gln Val Ser 725	Asp Leu Glu Lys Ile Thr 730	Thr Gln Val Tyr Met 735	Leu
Phe Lys Ser Ser Ser 740	Tyr Glu Glu Leu Ala 745	Leu Lys Val Ser Ser 750	Tyr
Gln Ile Asn Gln Val Ala 755	Leu Lys Val Met Ala 760	Leu Ser Asp Glu Lys 765	
Phe Cys Glu Glu Lys 770	Arg Leu Leu Arg Lys 775	Leu Val Asn Lys Ala 780	Asn
Gln Leu Leu Glu Ala Arg 785	Asn Leu Leu Val Gly 790	Gly Gly Asn Phe Glu Thr 795	800
Thr Gln Asn Trp Val 805	Leu Gly Thr Asn Ala 810	Tyr Ile Asn Tyr Asp Ser 815	
Phe Leu Phe Asn Gly 820	Asn Tyr Leu Ser Leu 825	Gln Pro Ala Ser Gly Phe 830	
Phe Thr Ser Tyr Ala Tyr 835	Gln Lys Ile Asp Glu Ser 840	Thr Leu Lys Pro 845	
Tyr Thr Arg Tyr Lys Val 850	Ser Gly Phe Ile Gly 855	Gln Ser Asn Gln Val 860	
Glu Leu Ile Ile Ser Arg 865	Tyr Gly Lys Glu Ile 870	Asp Lys Ile Leu Asn 875	880
Val Pro Tyr Ala Gly 885	Pro Leu Pro Ile Thr 890	Ala Asp Ala Ser Ile Thr 895	
Cys Cys Ala Pro Glu Ile 900	Asp Gln Cys Asp Gly 905	Gly Gln Ser Asp Ser 910	
His Phe Phe Asn Tyr Ser 915	Ile Asp Val Gly Ala 920	Leu His Pro Glu Leu 925	
Asn Pro Gly Ile Glu Ile 930	Gly Leu Lys Ile Val 935	Gln Ser Asn Gly Tyr 940	
Ile Thr Ile Ser Asn Leu 945	Glu Ile Ile Glu Glu 950	Arg Pro Leu Thr Glu 955	960
Met Glu Ile Gln Ala Val 965	Asn Arg Lys Asp Gln 970	Lys Trp Lys Arg Glu 975	
Lys Leu Leu Glu Cys Ala 980	Ser Val Ser Glu Leu 985	Leu Gln Pro Ile Ile 990	
Asn Gln Ile Asp Ser Leu 995	Phe Lys Asp Ala Asn 1000	Trp Tyr Asn Asp Ile 1005	
Leu Pro His Val Thr Tyr 1010	Gln Thr Leu Lys Asn 1015	Ile Ile Val Pro Asp 1020	
Leu Pro Lys Leu Lys His 1025	Trp Phe Ile Asp His 1030	Leu Pro Gly Glu Tyr 1035	1040

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His Glu Ile Glu Gln Lys Met Lys Glu Ala Leu Lys His Ala Phe Thr
1045 1050 1055

Gln Leu Asp Glu Lys Asn Leu Ile His Asn Gly His Phe Ala Thr Asn
1060 1065 1070

Leu Ile Asp Trp Gln Val Glu Gly Asp Ala Arg Met Lys Val Leu Glu
1075 1080 1085

Asn Asn Ala Leu Ala Leu Gln Leu Ser Asn Trp Asp Ser Ser Val Ser
1090 1095 1100

Gln Ser Ile Asp Ile Leu Glu Phe Asp Glu Asp Lys Ala Tyr Lys Leu
1105 1110 1115 1120

Arg Val Tyr Ala Gln Gly Ser Gly Thr Ile Gln Phe Gly Asn Cys Glu
1125 1130 1135

Asp Glu Ala Ile Gln Phe Asn Thr Asn Ser Phe Val Tyr Lys Glu Lys
1140 1145 1150

Ile Ile Tyr Phe Asp Thr Pro Ser Ile Asn Leu His Ile Gln Ser Glu
1155 1160 1165

Gly Ser Glu Phe Val Val Ser Ser Ile Asp Leu Val Glu Leu Ser Asp
1170 1175 1180

Asp Glu
1185

<210> SEQ ID NO 14
<211> LENGTH: 2190
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: axmi-031(truncated)
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2190)

<400> SEQUENCE: 14

atg tcg tac tac cat cac cat cac cat cac ctc gaa tca aca agt ttg	48
Met Ser Tyr Tyr His His His His His His Leu Glu Ser Thr Ser Leu	
1 5 10 15	
tac aaa aaa gca ggc ttc att gaa gga cgt atg gat tgt aat tta caa	96
Tyr Lys Lys Ala Gly Phe Ile Glu Gly Arg Met Asp Cys Asn Leu Gln	
20 25 30	
tca caa caa aat att cca tat aat gta tta gca ata cca gta tct aat	144
Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu Ala Ile Pro Val Ser Asn	
35 40 45	
gtt aat tcg ttg act gat aca gtt gga gat tta aaa aaa gca tgg gaa	192
Val Asn Ser Leu Thr Asp Thr Val Gly Asp Leu Lys Lys Ala Trp Glu	
50 55 60	
gaa ttt caa aaa act ggt tct ttt tca tta aca gct tta caa caa gga	240
Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu Thr Ala Leu Gln Gln Gly	
65 70 75 80	
ttt tct gct tca caa gga gga aca ttc aat tat tta aca tta cta caa	288
Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn Tyr Leu Thr Leu Leu Gln	
85 90 95	
tca gga ata tca tta gct ggt tct ttt gtt cct gga ggt act ttt gta	336
Ser Gly Ile Ser Leu Ala Gly Ser Phe Val Pro Gly Gly Thr Phe Val	
100 105 110	
gca cct att att aat atg gtt att ggt tgg tta tgg cca cat aaa aac	384
Ala Pro Ile Ile Asn Met Val Ile Gly Trp Leu Trp Pro His Lys Asn	
115 120 125	

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aaa aat gcg gat aca gaa aat tta ata aat tta att gat tca gaa att	432
Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn Leu Ile Asp Ser Glu Ile	
130 135 140	
caa aaa caa tta aac aaa gct tta tta gat gca gat aga aat gag tgg	480
Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp Ala Asp Arg Asn Glu Trp	
145 150 155 160	
agc tct tat tta gaa tct ata ttt gat tct tca aat aac cta aat ggt	528
Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser Ser Asn Asn Leu Asn Gly	
165 170 175	
gca att gta gat gca cag tgg tca ggc act gta aat act aca aat aga	576
Ala Ile Val Asp Ala Gln Trp Ser Gly Thr Val Asn Thr Thr Asn Arg	
180 185 190	
aca cta aga aat cca aca gaa tca gat tat aca aat gtt gtt aca aat	624
Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr Thr Asn Val Val Thr Asn	
195 200 205	
ttt att gca gcg gat ggt gac att gca aat aat gaa aat cac ata atg	672
Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn Asn Glu Asn His Ile Met	
210 215 220	
aat ggc aac ttt gac gta gct gca gca cct tat ttt gtt ata gga gca	720
Asn Gly Asn Phe Asp Val Ala Ala Ala Pro Tyr Phe Val Ile Gly Ala	
225 230 235 240	
aca gca cgt ttt gca gca atg caa tct tat att aaa ttt tgt aat gct	768
Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr Ile Lys Phe Cys Asn Ala	
245 250 255	
tgg att gat aaa gtt gga ttg agt gac gca cag ctt act aca caa aag	816
Trp Ile Asp Lys Val Gly Leu Ser Asp Ala Gln Leu Thr Thr Gln Lys	
260 265 270	
gct aat tta gat cgc acg aaa caa aat atg cgt aat gca att ctt aac	864
Ala Asn Leu Asp Arg Thr Lys Gln Asn Met Arg Asn Ala Ile Leu Asn	
275 280 285	
tat aca caa caa gtt atg aaa gtt ttt aaa gat tcc aaa aat atg cct	912
Tyr Thr Gln Gln Val Met Lys Val Phe Lys Asp Ser Lys Asn Met Pro	
290 295 300	
aca ata ggt act aat aaa ttt agt gtt gat acc tat aat gta tat att	960
Thr Ile Gly Thr Asn Lys Phe Ser Val Asp Thr Tyr Asn Val Tyr Ile	
305 310 315 320	
aaa gga atg aca tta aat gtt tta gat att gta gca ata tgg cct tca	1008
Lys Gly Met Thr Leu Asn Val Leu Asp Ile Val Ala Ile Trp Pro Ser	
325 330 335	
tta tat cca gat gat tat act tca caa aca gcc tta gaa caa aca cgt	1056
Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr Ala Leu Glu Gln Thr Arg	
340 345 350	
gtc act ttt tca aat atg gtt ggc caa gaa gaa ggt aca gat gga agc	1104
Val Thr Phe Ser Asn Met Val Gly Gln Glu Glu Gly Thr Asp Gly Ser	
355 360 365	
cta aga att tac aat act ttt gat tct ttt agt tat caa cat agt cca	1152
Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe Ser Tyr Gln His Ser Pro	
370 375 380	
ata cct aat aat aat gtt aat tta att tct tat tat aat gat gaa tta	1200
Ile Pro Asn Asn Asn Val Asn Leu Ile Ser Tyr Tyr Asn Asp Glu Leu	
385 390 395 400	
caa aat cta gaa tta gga gta tat acc cct cct aaa aaa gga agt gga	1248
Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro Pro Lys Lys Gly Ser Gly	
405 410 415	
tac tct tat cct tat gga ttt gtt tta aat tat gca aac agt aaa tat	1296
Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn Tyr Ala Asn Ser Lys Tyr	
420 425 430	

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aaa tat ggt gat agc aat gat cca gaa tct cta gga gga tta tct aca	1344
Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser Leu Gly Gly Leu Ser Thr	
435 440 445	
cta tct gca cct ata caa caa gtt aat gca gca act caa aac agt aaa	1392
Leu Ser Ala Pro Ile Gln Gln Val Asn Ala Ala Thr Gln Asn Ser Lys	
450 455 460	
tat cta gat gga gaa atc cta aat gga ata gga gca tcc tta cct ggt	1440
Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile Gly Ala Ser Leu Pro Gly	
465 470 475 480	
tat tgt act aca gga tgt tca cca aca gaa cca cct ttt agt tgt act	1488
Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu Pro Pro Phe Ser Cys Thr	
485 490 495	
tct acc gct aat ggc tat aaa gca agc tgt aat cct tca gat aca aat	1536
Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys Asn Pro Ser Asp Thr Asn	
500 505 510	
caa aaa att aac gct tta tat cct ttt aca caa gct aat gta aag gga	1584
Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr Gln Ala Asn Val Lys Gly	
515 520 525	
aac aca gga aaa tta gga gta ctg gca agt ctt gtt tca tat gat tta	1632
Asn Thr Gly Lys Leu Gly Val Leu Ala Ser Leu Val Ser Tyr Asp Leu	
530 535 540	
aat cct aaa aat gta ttt ggt gaa tta gat tca gat aca aat aat gtt	1680
Asn Pro Lys Asn Val Phe Gly Glu Leu Asp Ser Asp Thr Asn Asn Val	
545 550 555 560	
atc tta aaa gga att cct gca gaa aaa gga tat ttt cct aat aat gcg	1728
Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly Tyr Phe Pro Asn Asn Ala	
565 570 575	
cgt cct act gtt gta aaa gaa tgg att aat ggt gca agt gct gta cca	1776
Arg Pro Thr Val Val Lys Glu Trp Ile Asn Gly Ala Ser Ala Val Pro	
580 585 590	
ctt gat tca gga aat acc tta ttt atg acg gct acg aat tta aca gct	1824
Leu Asp Ser Gly Asn Thr Leu Phe Met Thr Ala Thr Asn Leu Thr Ala	
595 600 605	
act caa tat aga att aga ata cgt tat gca aat cca aat tca aat act	1872
Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala Asn Pro Asn Ser Asn Thr	
610 615 620	
caa atc ggt gta cga att aca caa aat ggt tct cta att tcc agt agt	1920
Gln Ile Gly Val Arg Ile Thr Gln Asn Gly Ser Leu Ile Ser Ser Ser	
625 630 635 640	
aat cta aca ctt tat agt act act gat atg aat aat act tta cca cta	1968
Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met Asn Asn Thr Leu Pro Leu	
645 650 655	
aat gta tat gta ata gga gaa aat gga aat tat aca ctt caa gat tta	2016
Asn Val Tyr Val Ile Gly Glu Asn Gly Asn Tyr Thr Leu Gln Asp Leu	
660 665 670	
tat aat act act aat gtt tta tca aca gga gat att aca tta caa att	2064
Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly Asp Ile Thr Leu Gln Ile	
675 680 685	
aca gga gga gat caa aaa ata ttt att gat cga ata gaa ttt gtt cct	2112
Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp Arg Ile Glu Phe Val Pro	
690 695 700	
act atg cct gta cct ggt aat act aac aac aat aac ggt aat aat aac	2160
Thr Met Pro Val Pro Gly Asn Thr Asn Asn Asn Asn Gly Asn Asn Asn	
705 710 715 720	
ggt aat aat aat ccc cca cac cac gtc tag	2190
Gly Asn Asn Asn Pro Pro His His Val *	
725	

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<210> SEQ ID NO 15
<211> LENGTH: 729
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: AXMI-031(TRUNCATED)

<400> SEQUENCE: 15

Met Ser Tyr Tyr His His His His His Leu Glu Ser Thr Ser Leu
 1          5          10          15

Tyr Lys Lys Ala Gly Phe Ile Glu Gly Arg Met Asp Cys Asn Leu Gln
 20          25          30

Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu Ala Ile Pro Val Ser Asn
 35          40          45

Val Asn Ser Leu Thr Asp Thr Val Gly Asp Leu Lys Lys Ala Trp Glu
 50          55          60

Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu Thr Ala Leu Gln Gln Gly
 65          70          75          80

Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn Tyr Leu Thr Leu Leu Gln
 85          90          95

Ser Gly Ile Ser Leu Ala Gly Ser Phe Val Pro Gly Gly Thr Phe Val
100          105          110

Ala Pro Ile Ile Asn Met Val Ile Gly Trp Leu Trp Pro His Lys Asn
115          120          125

Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn Leu Ile Asp Ser Glu Ile
130          135          140

Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp Ala Asp Arg Asn Glu Trp
145          150          155          160

Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser Ser Asn Asn Leu Asn Gly
165          170          175

Ala Ile Val Asp Ala Gln Trp Ser Gly Thr Val Asn Thr Thr Asn Arg
180          185          190

Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr Thr Asn Val Val Thr Asn
195          200          205

Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn Asn Glu Asn His Ile Met
210          215          220

Asn Gly Asn Phe Asp Val Ala Ala Ala Pro Tyr Phe Val Ile Gly Ala
225          230          235          240

Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr Ile Lys Phe Cys Asn Ala
245          250          255

Trp Ile Asp Lys Val Gly Leu Ser Asp Ala Gln Leu Thr Thr Gln Lys
260          265          270

Ala Asn Leu Asp Arg Thr Lys Gln Asn Met Arg Asn Ala Ile Leu Asn
275          280          285

Tyr Thr Gln Gln Val Met Lys Val Phe Lys Asp Ser Lys Asn Met Pro
290          295          300

Thr Ile Gly Thr Asn Lys Phe Ser Val Asp Thr Tyr Asn Val Tyr Ile
305          310          315          320

Lys Gly Met Thr Leu Asn Val Leu Asp Ile Val Ala Ile Trp Pro Ser
325          330          335

Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr Ala Leu Glu Gln Thr Arg
340          345          350

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<210> SEQ ID NO 16
<211> LENGTH: 3558
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: axmi-031(m1)
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gca ata cca gta tct aat gtt aat tcg ttg act gat aca gtt gga gat	96
Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp	
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tta aaa aaa gca tgg gaa gaa ttt caa aaa act ggt tct ttt tca tta	144
Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu	
35 40 45	
aca gct tta caa caa gga ttt tct gct tca caa gga gga aca ttc aat	192
Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn	
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tat tta aca tta cta caa tca gga ata tca tta gct ggt tct ttt gtt	240
Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val	
65 70 75 80	
cct gga ggt act ttt gta gca cct att att aat atg gtt att ggt tgg	288
Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp	
85 90 95	
tta tgg cca cat aaa aac aaa aat gcg gat aca gaa aat tta ata aat	336
Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn	
100 105 110	
tta att gat tca gaa att caa aaa caa tta aac aaa gct tta tta gat	384
Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp	
115 120 125	
gca gat aga aat gag tgg agc tct tat tta gaa tct ata ttt gat tct	432
Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser	
130 135 140	
tca aat aac cta aat ggt gca att gta gat gca cag tgg tca ggc act	480
Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr	
145 150 155 160	
gta aat act aca aat aga aca cta aga aat cca aca gaa tca gat tat	528
Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr	
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Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn	
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Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Pro	
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Tyr Phe Ala Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr	
210 215 220	
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Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala	
225 230 235 240	
cag ctt act aca caa aag gct aat tta gat cgc acg aaa caa aat atg	768
Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met	
245 250 255	
cgt aat gca att ctt aac tat aca caa caa gtt atg aaa gtt ttt aaa	816
Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys	
260 265 270	

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acc tat aat gta tat att aaa gga atg aca tta aat gtt tta gat att Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile 290 295 300	912
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cct aaa aaa gga agt gga tac tct tat cct tat gga ttt gtt tta aat Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn 385 390 395 400	1200
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gca act caa aac agt aaa tat cta gat gga gaa atc cta aat gga ata Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile 435 440 445	1344
gga gca tcc tta cct ggt tat tgt act aca gga tgt tca cca aca gaa Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu 450 455 460	1392
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Cys Ala Pro Glu Ile Gly Gln Cys Asp 905 Gly Glu Gln Ser Asp Ser His 910	
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Phe Phe Asn Tyr Ser Ile Asp Val Gly Ala Leu His Pro Glu Leu Asn 915 920 925	
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Val Tyr Ala Gln Gly Ser Gly Thr Ile Gln Phe Gly Asn Cys Glu Asp 1125 1130 1135	
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Val Tyr Phe Asp Thr Pro Ser Val Asn Leu His Ile Gln Ser Glu Gly 1155 1160 1165	
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 Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val
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 Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp
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 Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn
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 Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp
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 Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser
 130 135 140
 Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr
 145 150 155 160
 Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr
 165 170 175
 Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn
 180 185 190
 Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro
 195 200 205
 Tyr Phe Ala Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr
 210 215 220
 Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala
 225 230 235 240
 Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met
 245 250 255
 Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys
 260 265 270
 Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp
 275 280 285
 Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile
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 305 310 315 320
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Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn	
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Gln	Ala	Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	Ser	
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Ala	Thr	Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr	Ala	
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Gln	Val	Ser	Asp	Leu	Glu	Lys	Ile	Thr	Thr	Gln	Val	Tyr	Met	Leu	Phe	
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Cys	Glu	Glu	Lys	Asn	Val	Leu	Arg	Lys	Leu	Val	Asn	Lys	Ala	Lys	Gln
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Leu	Leu	Glu	Ala	Ser	Asn	Leu	Leu	Val	Gly	Gly	Asn	Phe	Glu	Thr	Thr
785					790					795					800
Gln	Asn	Trp	Val	Leu	Gly	Thr	Asn	Ala	Tyr	Ile	Asn	Tyr	Asp	Ser	Phe
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Leu	Phe	Asn	Gly	Asn	Tyr	Leu	Ser	Leu	Gln	Pro	Ala	Ser	Gly	Phe	Phe
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Thr	Ser	Tyr	Ala	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Thr	Leu	Lys	Pro	Tyr
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Thr	Arg	Tyr	Lys	Val	Ser	Gly	Phe	Ile	Gly	Gln	Ser	Asn	Gln	Val	Glu
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Cys	Ala	Pro	Glu	Ile	Gly	Gln	Cys	Asp	Gly	Glu	Gln	Ser	Asp	Ser	His
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Gln	Ile	Asp	Ser	Leu	Phe	Lys	Asp	Gly	Asn	Trp	Tyr	Asn	Asp	Ile	Leu
	995						1000					1005			
Pro	His	Val	Thr	Tyr	Gln	Asp	Leu	Lys	Asn	Ile	Ile	Ile	Pro	Glu	Leu
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Glu	Ile	Glu	Gln	Lys	Met	Lys	Glu	Ala	Leu	Lys	Tyr	Ala	Phe	Thr	Gln
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Leu	Asp	Glu	Lys	Asn	Leu	Ile	His	Asn	Gly	His	Phe	Thr	Thr	Asn	Leu
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Ser	Ile	Asn	Ile	Leu	Glu	Phe	Asp	Glu	Asp	Lys	Ala	Tyr	Lys	Leu	Arg
	1105				1110					1115					1120
Val	Tyr	Ala	Gln	Gly	Ser	Gly	Thr	Ile	Gln	Phe	Gly	Asn	Cys	Glu	Asp
			1125						1130					1135	

Gln
1185

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<210> SEQ ID NO 18
<211> LENGTH: 2112
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: axmi-031(m1)truncated
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)...(2112)
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<400> SEQUENCE: 18

atg	gat	tgt	aat	tta	caa	tca	caa	caa	aat	att	cca	tat	aat	gta	tta	48
Met	Asp	Cys	Asn	Leu	Gln	Ser	Gln	Gln	Asn	Ile	Pro	Tyr	Asn	Val	Leu	
1			5						10					15		
gca	ata	cca	gta	tct	aat	gtt	aat	tcg	ttg	act	gat	aca	gtt	gga	gat	96
Ala	Ile	Pro	Val	Ser	Asn	Val	Asn	Ser	Leu	Thr	Asp	Thr	Val	Gly	Asp	
			20					25					30			
tta	aaa	aaa	gca	tggt	gaa	gaa	ttt	caa	aaa	act	ggt	tct	ttt	tca	tta	144
Leu	Lys	Lys	Ala	Trp	Glu	Glu	Phe	Gln	Lys	Thr	Gly	Ser	Phe	Ser	Leu	
		35					40					45				
aca	gct	tta	caa	caa	gga	ttt	tct	gct	tca	caa	gga	gga	aca	ttc	aat	192
Thr	Ala	Leu	Gln	Gln	Gly	Phe	Ser	Ala	Ser	Gln	Gly	Gly	Thr	Phe	Asn	
	50					55					60					
tat	tta	aca	tta	cta	caa	tca	gga	ata	tca	tta	gct	ggt	tct	ttt	gtt	240
Tyr	Leu	Thr	Leu	Leu	Gln	Ser	Gly	Ile	Ser	Leu	Ala	Gly	Ser	Phe	Val	
	65			70						75					80	
cct	gga	ggt	act	ttt	gta	gca	cct	att	att	aat	atg	ggt	att	ggt	tggt	288
Pro	Gly	Gly	Thr	Phe	Val	Ala	Pro	Ile	Ile	Asn	Met	Val	Ile	Gly	Trp	
			85						90					95		
tta	tggt	cca	cat	aaa	aac	aaa	aat	gcg	gat	aca	gaa	aat	tta	ata	aat	336
Leu	Trp	Pro	His	Lys	Asn	Lys	Asn	Ala	Asp	Thr	Glu	Asn	Leu	Ile	Asn	
			100					105					110			
tta	att	gat	tca	gaa	att	caa	aaa	caa	tta	aac	aaa	gct	tta	tta	gat	384
Leu	Ile	Asp	Ser	Glu	Ile	Gln	Lys	Gln	Leu	Asn	Lys	Ala	Leu	Leu	Asp	
		115				120					125					
gca	gat	aga	aat	gag	tggt	agc	tct	tat	tta	gaa	tct	ata	ttt	gat	tct	432
Ala	Asp	Arg	Asn	Glu	Trp	Ser	Ser	Tyr	Leu	Glu	Ser	Ile	Phe	Asp	Ser	
	130					135					140					
tca	aat	aac	cta	aat	ggt	gca	att	gta	gat	gca	cag	tggt	tca	ggc	act	480
Ser	Asn	Asn	Leu	Asn	Gly	Ala	Ile	Val	Asp	Ala	Gln	Trp	Ser	Gly	Thr	
	145			150						155				160		
gta	aat	act	aca	aat	aga	aca	cta	aga	aat	cca	aca	gaa	tca	gat	tat	528
Val	Asn	Thr	Thr	Asn	Arg	Thr	Leu	Arg	Asn	Pro	Thr	Glu	Ser	Asp	Tyr	
			165					170					175			
aca	aat	gtt	gtt	aca	aat	ttt	att	gca	gcg	gat	ggt	gac	att	gca	aat	576
Thr	Asn	Val	Val	Thr	Asn	Phe	Ile	Ala	Ala	Asp	Gly	Asp	Ile	Ala	Asn	
			180					185					190			
aat	gaa	aat	cac	ata	atg	aat	ggc	aac	ttt	gac	gta	gct	gca	gca	cct	624
Asn	Glu	Asn	His	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala	Ala	Ala	Pro	
		195				200										

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tat ttt gct ata gga gca aca gca cgt ttt gca gca atg caa tct tat	672
Tyr Phe Ala Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr	
210 215 220	
att aaa ttt tgt aat gct tgg att gat aaa gtt gga ttg agt gac gca	720
Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala	
225 230 235 240	
cag ctt act aca caa aag gct aat tta gat cgc acg aaa caa aat atg	768
Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met	
245 250 255	
cgt aat gca att ctt aac tat aca caa caa gtt atg aaa gtt ttt aaa	816
Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys	
260 265 270	
gat tcc aaa aat atg cct aca ata ggt act aat aaa ttt agt gtt gat	864
Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp	
275 280 285	
acc tat aat gta tat att aaa gga atg aca tta aat gtt tta gat att	912
Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile	
290 295 300	
gta gca ata tgg cct tca tta tat cca gat gat tat act tca caa aca	960
Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr	
305 310 315 320	
gcc tta gaa caa aca cgt gtc act ttt tca aat atg gtt ggc caa gaa	1008
Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu	
325 330 335	
gaa ggt aca gat gga agc cta aga att tac aat act ttt gat tct ttt	1056
Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe	
340 345 350	
agt tat caa cat agt cca ata cct aat aat aat gtt aat tta att tct	1104
Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser	
355 360 365	
tat tat aat gat gaa tta caa aat cta gaa tta gga gta tat acc cct	1152
Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro	
370 375 380	
cct aaa aaa gga agt gga tac tct tat cct tat gga ttt gtt tta aat	1200
Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn	
385 390 395 400	
tat gca aac agt aaa tat aaa tat ggt gat agc aat gat cca gaa tct	1248
Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser	
405 410 415	
cta gga gga tta tct aca cta tct gca cct ata caa caa gtt aat gca	1296
Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala	
420 425 430	
gca act caa aac agt aaa tat cta gat gga gaa atc cta aat gga ata	1344
Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile	
435 440 445	
gga gca tcc tta cct ggt tat tgt act aca gga tgt tca cca aca gaa	1392
Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu	
450 455 460	
cca cct ttt agt tgt act tct acc gct aat ggc tat aaa gca agc tgt	1440
Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys	
465 470 475 480	
aat cct tca gat aca aat caa aaa att aac gct tta tat cct ttt aca	1488
Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr	
485 490 495	
caa gct aat gta aag gga aac aca gga aaa tta gga gta ctg gca agt	1536
Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser	
500 505 510	

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ctt gtt tca tat gat tta aat cct aaa aat gta ttt ggt gag tta gat      1584
Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp
      515                      520                      525

tca gat aca aat aat gtt atc tta aaa gga att cct gca gaa aaa gga      1632
Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly
      530                      535                      540

tat ttt cct aat aat gcg cgt cct act gtt gta aaa gaa tgg att aat      1680
Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn
545                      550                      555                      560

ggt gca agt gct gta cca ctt gat tca gga aat acc tta ttt atg acg      1728
Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr
      565                      570                      575

gct acg aat tta aca gct act caa tat aga att aga ata cgt tat gca      1776
Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala
      580                      585                      590

aat cca aat tca aat act caa atc ggt gta cga att aca caa aat ggt      1824
Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly
      595                      600                      605

tct cta att tcc agt agt aat cta aca ctt tat agt act act gat atg      1872
Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met
      610                      615                      620

aat aat act tta cca cta aat gta tat gta ata gga gaa aat gga aat      1920
Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn
625                      630                      635                      640

tat aca ctt caa gat tta tat aat act act aat gtt tta tca aca gga      1968
Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly
      645                      650                      655

gat att aca tta caa att aca gga gga gat caa aaa ata ttt att gat      2016
Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp
      660                      665                      670

cga ata gaa ttt gtt cct act atg cct gta cct ggt aat act aac aac      2064
Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn Asn
      675                      680                      685

aat aac ggt aat aat aac ggt aat aat aat ccc cca cac cac gtc tag      2112
Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val *
      690                      695                      700

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<210> SEQ ID NO 19
<211> LENGTH: 703
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: AXMI-031(M1)TRUNCATED

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<400> SEQUENCE: 19

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Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp
      20              25              30

Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu
      35              40              45

Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn
      50              55              60

Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val
      65              70              75              80

Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp
      85              90              95

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Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn
 100 105 110
 Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp
 115 120 125
 Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser
 130 135 140
 Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr
 145 150 155 160
 Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr
 165 170 175
 Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn
 180 185 190
 Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro
 195 200 205
 Tyr Phe Ala Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr
 210 215 220
 Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala
 225 230 235 240
 Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met
 245 250 255
 Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys
 260 265 270
 Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp
 275 280 285
 Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile
 290 295 300
 Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr
 305 310 315 320
 Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu
 325 330 335
 Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe
 340 345 350
 Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser
 355 360 365
 Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro
 370 375 380
 Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn
 385 390 395 400
 Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser
 405 410 415
 Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala
 420 425 430
 Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile
 435 440 445
 Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu
 450 455 460
 Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys
 465 470 475 480
 Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr
 485 490 495

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Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser
500 505 510

Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp
515 520 525

Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly
530 535 540

Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn
545 550 555 560

Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr
565 570 575

Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala
580 585 590

Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly
595 600 605

Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met
610 615 620

Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn
625 630 635 640

Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly
645 650 655

Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp
660 665 670

Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn Asn
675 680 685

Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val
690 695 700

<210> SEQ ID NO 20
 <211> LENGTH: 2219
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: axmi-031(A-D)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(2216)

<400> SEQUENCE: 20

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1 5 10 15	
gca ata cca gta tct aat gtt aat tcg ttg act gat aca gtt gga gat	96
Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp	
20 25 30	
tta aaa aaa gca tgg gaa gaa ttt caa aaa act ggt tct ttt tca tta	144
Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu	
35 40 45	
aca gct tta caa caa gga ttt tct gct tca caa gga gga aca ttc aat	192
Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn	
50 55 60	
tat tta aca tta cta caa tca gga ata tca tta gct ggt tct ttt gtt	240
Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val	
65 70 75 80	
cct gga ggt act ttt gta gca cct att att aat atg gtt att ggt tgg	288
Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp	
85 90 95	

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tta tgg cca cat aaa aac aaa aat gcg gat aca gaa aat tta ata aat	336
Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn	
100 105 110	
tta att gat tca gaa att caa aaa caa tta aac aaa gct tta tta gat	384
Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp	
115 120 125	
gca gat aga aat gag tgg agc tct tat tta gaa tct ata ttt gat tct	432
Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser	
130 135 140	
tca aat aac cta aat ggt gca att gta gat gca cag tgg tca ggc act	480
Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr	
145 150 155 160	
gta aat act aca aat aga aca cta aga aat cca aca gaa tca gat tat	528
Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr	
165 170 175	
aca aat gtt gtt aca aat ttt att gca gcg gat ggt gac att gca aat	576
Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn	
180 185 190	
aat gaa aat cac ata atg aat ggc aac ttt gac gta gct gca gca cct	624
Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro	
195 200 205	
tat ttt gtt ata gga gca aca gca cgt ttt gca gca atg caa tct tat	672
Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr	
210 215 220	
att aaa ttt tgt aat gct tgg att gat aaa gtt gga ttg agt gac gca	720
Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala	
225 230 235 240	
cag ctt act aca caa aag gct aat tta gat cgc acg aaa caa aat atg	768
Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met	
245 250 255	
cgt aat gca att ctt aac tat aca caa caa gtt atg aaa gtt ttt aaa	816
Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys	
260 265 270	
gat tcc aaa aat atg cct aca ata ggt act aat aaa ttt agt gtt gat	864
Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp	
275 280 285	
acc tat aat gta tat att aaa gga atg aca tta aat gtt tta gat att	912
Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile	
290 295 300	
gta gca ata tgg cct tca tta tat cca gat gat tat act tca caa aca	960
Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr	
305 310 315 320	
gcc tta gaa caa aca cgt gtc act ttt tca aat atg gtt ggc caa gaa	1008
Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu	
325 330 335	
gaa ggt aca gat gga agc cta aga att tac aat act ttt gat tct ttt	1056
Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe	
340 345 350	
agt tat caa cat agt cca ata cct aat aat aat gtt aat tta att tct	1104
Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser	
355 360 365	
tat tat aat gat gaa tta caa aat cta gaa tta gga gta tat acc cct	1152
Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro	
370 375 380	
cct aaa aaa gga agt gga tac tct tat cct tat gga ttt gtt tta aat	1200
Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn	
385 390 395 400	

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tat gca aac agt aaa tat aaa tat ggt gat agc aat gat cca gaa tct	1248
Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser	
405 410 415	
cta gga gga tta tct aca cta tct gca cct ata caa caa gtt aat gca	1296
Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala	
420 425 430	
gca act caa aac agt aaa tat cta gat gga gaa atc cta aat gga ata	1344
Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile	
435 440 445	
gga gca tcc tta cct ggt tat tgt act aca gga tgt tca cca aca gaa	1392
Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu	
450 455 460	
cca cct ttt agt tgt act tct acc gct aat ggc tat aaa gca agc tgt	1440
Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys	
465 470 475 480	
aat cct tca gat aca aat caa aaa att aac gct tta tat cct ttt aca	1488
Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr	
485 490 495	
caa gct aat gta aag gga aac aca gga aaa tta gga gta ctg gca agt	1536
Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser	
500 505 510	
ctt gtt tca tat gat tta aat cct aaa aat gta ttt ggt gaa tta gat	1584
Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp	
515 520 525	
tca gat aca aat aat gtt atc tta aaa gga att cct gca gaa aaa gga	1632
Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly	
530 535 540	
tat ttt cct aat aat gcg cgt cct act gtt gta aaa gaa tgg att aat	1680
Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn	
545 550 555 560	
ggt gca agt gct gta cca ctt gat tca gga aat acc tta ttt atg acg	1728
Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr	
565 570 575	
gct acg aat tta aca gct act caa tat aga att aga ata cgt tat gca	1776
Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala	
580 585 590	
aat cca aat tca aat act caa atc ggt gta cga att aca caa aat ggt	1824
Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly	
595 600 605	
tct cta att tcc agt agt aat cta aca ctt tat agt act act gat atg	1872
Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met	
610 615 620	
aat aat act tta cca cta aat gta tat gta ata gga gaa aat gga aat	1920
Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn	
625 630 635 640	
tat aca ctt caa gat tta tat aat act act aat gtt tta tca aca gga	1968
Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly	
645 650 655	
gat att aca tta caa att aca gga gga gat caa aaa ata ttt att gat	2016
Asp Ile Thr Leu Gln Ile Thr Gly Asp Gln Lys Ile Phe Ile Asp	
660 665 670	
cga ata gaa ttt gtt cct act atg cct gta cct ggt aat act aac aac	2064
Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn Asn	
675 680 685	
aat aac ggt aat aat aac ggt aat aat aat ccc cca cac cac gtt tgt	2112
Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val Cys	
690 695 700	

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gca ata gct ggt aca caa caa tct tgt tct gga ccg ccc aaa ttt gaa	2160
Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe Glu	
705 710 715 720	

caa gta agt gat tta gaa aaa att aca aca caa gta tat atg tta ttc	2208
Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu Phe	
725 730 735	

aaa tct ta tag	2219
Lys Ser	

<210> SEQ ID NO 21
 <211> LENGTH: 738
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: AXMI-031(A-D)

<400> SEQUENCE: 21

Met Asp Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu	
1 5 10 15	
Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp	
20 25 30	
Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu	
35 40 45	
Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn	
50 55 60	
Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val	
65 70 75 80	
Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp	
85 90 95	
Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn	
100 105 110	
Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp	
115 120 125	
Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser	
130 135 140	
Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr	
145 150 155 160	
Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr	
165 170 175	
Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn	
180 185 190	
Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro	
195 200 205	
Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr	
210 215 220	
Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala	
225 230 235 240	
Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met	
245 250 255	
Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys	
260 265 270	
Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp	
275 280 285	
Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile	

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290	295	300
Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr 305 310 315 320		
Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu 325 330 335		
Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe 340 345 350		
Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser 355 360 365		
Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro 370 375 380		
Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn 385 390 395 400		
Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser 405 410 415		
Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala 420 425 430		
Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile 435 440 445		
Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu 450 455 460		
Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys 465 470 475 480		
Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr 485 490 495		
Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser 500 505 510		
Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp 515 520 525		
Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly 530 535 540		
Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn 545 550 555 560		
Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr 565 570 575		
Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala 580 585 590		
Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly 595 600 605		
Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met 610 615 620		
Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn 625 630 635 640		
Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly 645 650 655		
Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp 660 665 670		
Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn Asn 675 680 685		
Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val Cys 690 695 700		

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Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe Glu
 705 710 715 720
 Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu Phe
 725 730 735

Lys Ser

<210> SEQ ID NO 22
 <211> LENGTH: 2015
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: axmi-031(B-C)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(2012)

<400> SEQUENCE: 22

atg gca ata cca gta tct aat gtt aat tcg ttg act gat aca gtt gga	48
Met Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly	
1 5 10 15	
gat tta aaa aaa gca tgg gaa gaa ttt caa aaa act ggt tct ttt tca	96
Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser	
20 25 30	
tta aca gct tta caa caa gga ttt tct gct tca caa gga gga aca ttc	144
Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe	
35 40 45	
aat tat tta aca tta cta caa tca gga ata tca tta gct ggt tct ttt	192
Asn Tyr Leu Thr Leu Leu Ser Gly Ile Ser Leu Ala Gly Ser Phe	
50 55 60	
gtt cct gga ggt act ttt gta gca cct att att aat atg gtt att ggt	240
Val Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly	
65 70 75 80	
tggt tta tgg cca cat aaa aac aaa aat gcg gat aca gaa aat tta ata	288
Trp Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile	
85 90 95	
aat tta att gat tca gaa att caa aaa caa tta aac aaa gct tta tta	336
Asn Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu	
100 105 110	
gat gca gat aga aat gag tgg agc tct tat tta gaa tct ata ttt gat	384
Asp Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp	
115 120 125	
tct tca aat aac cta aat ggt gca att gta gat gca cag tgg tca ggc	432
Ser Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly	
130 135 140	
act gta aat act aca aat aga aca cta aga aat cca aca gaa tca gat	480
Thr Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp	
145 150 155 160	
tat aca aat gtt gtt aca aat ttt att gca gcg gat ggt gac att gca	528
Tyr Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala	
165 170 175	
aat aat gaa aat cac ata atg aat ggc aac ttt gac gta gct gca gca	576
Asn Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala	
180 185 190	
cct tat ttt gtt ata gga gca aca gca cgt ttt gca gca atg caa tct	624
Pro Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser	
195 200 205	
tat att aaa ttt tgt aat gct tgg att gat aaa gtt gga ttg agt gac	672
Tyr Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp	

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210	215	220	
gca cag ctt act aca caa aag gct aat tta gat cgc acg aaa caa aat			720
Ala Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn			
225	230	235	240
atg cgt aat gca att ctt aac tat aca caa caa gtt atg aaa gtt ttt			768
Met Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe			
	245	250	255
aaa gat tcc aaa aat atg cct aca ata ggt act aat aaa ttt agt gtt			816
Lys Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val			
	260	265	270
gat acc tat aat gta tat att aaa gga atg aca tta aat gtt tta gat			864
Asp Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp			
	275	280	285
att gta gca ata tgg cct tca tta tat cca gat gat tat act tca caa			912
Ile Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln			
	290	295	300
aca gcc tta gaa caa aca cgt gtc act ttt tca aat atg gtt ggc caa			960
Thr Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln			
	305	310	315
gaa gaa ggt aca gat gga agc cta aga att tac aat act ttt gat tct			1008
Glu Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser			
	325	330	335
ttt agt tat caa cat agt cca ata cct aat aat aat gtt aat tta att			1056
Phe Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile			
	340	345	350
tct tat tat aat gat gaa tta caa aat cta gaa tta gga gta tat acc			1104
Ser Tyr Tyr Asn Asp Glu Leu Ser Thr Leu Glu Leu Gly Val Tyr Thr			
	355	360	365
cct cct aaa aaa gga agt gga tac tct tat cct tat gga ttt gtt tta			1152
Pro Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu			
	370	375	380
aat tat gca aac agt aaa tat aaa tat ggt gat agc aat gat cca gaa			1200
Asn Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu			
	385	390	395
tct cta gga gga tta tct aca cta tct gca cct ata caa caa gtt aat			1248
Ser Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn			
	405	410	415
gca gca act caa aac agt aaa tat cta gat gga gaa atc cta aat gga			1296
Ala Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly			
	420	425	430
ata gga gca tcc tta cct ggt tat tgt act aca gga tgt tca cca aca			1344
Ile Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr			
	435	440	445
gaa cca cct ttt agt tgt act tct acc gct aat ggc tat aaa gca agc			1392
Glu Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser			
	450	455	460
tgt aat cct tca gat aca aat caa aaa att aac gct tta tat cct ttt			1440
Cys Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe			
	465	470	475
aca caa gct aat gta aag gga aac aca gga aaa tta gga gta ctg gca			1488
Thr Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala			
	485	490	495
agt ctt gtt tca tat gat tta aat cct aaa aat gta ttt ggt gaa tta			1536
Ser Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu			
	500	505	510
gat tca gat aca aat aat gtt atc tta aaa gga att cct gca gaa aaa			1584
Asp Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys			

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515	520	525	
gga tat ttt cct aat aat gcg cgt cct act gtt gta aaa gaa tgg att			1632
Gly Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile			
530	535	540	
aat ggt gca agt gct gta cca ctt gat tca gga aat acc tta ttt atg			1680
Asn Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met			
545	550	555	560
acg gct acg aat tta aca gct act caa tat aga att aga ata cgt tat			1728
Thr Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr			
565	570	575	
gca aat cca aat tca aat act caa atc ggt gta cga att aca caa aat			1776
Ala Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn			
580	585	590	
ggt tct cta att tcc agt agt aat cta aca ctt tat agt act act gat			1824
Gly Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp			
595	600	605	
atg aat aat act tta cca cta aat gta tat gta ata gga gaa aat gga			1872
Met Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly			
610	615	620	
aat tat aca ctt caa gat tta tat aat act act aat gtt tta tca aca			1920
Asn Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr			
625	630	635	640
gga gat att aca tta caa att aca gga gga gat caa aaa ata ttt att			1968
Gly Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile			
645	650	655	
gat cga ata gaa ttt gtt cct act atg cct gta cct ggt aat ta			2012
Asp Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn			
660	665	670	
tag			2015

<210> SEQ ID NO 23
 <211> LENGTH: 670
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: AXMI-031(B-C)

<400> SEQUENCE: 23

Met Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly
 1 5 10 15
 Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser
 20 25 30
 Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe
 35 40 45
 Asn Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe
 50 55 60
 Val Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly
 65 70 75 80
 Trp Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile
 85 90 95
 Asn Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu
 100 105 110
 Asp Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp
 115 120 125
 Ser Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly
 130 135 140

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Thr Val Asn Thr Thr	Asn Arg Thr Leu Arg	Asn Pro Thr Glu Ser Asp
145	150	155 160
Tyr Thr Asn Val Val	Thr Asn Phe Ile Ala Ala	Asp Gly Asp Ile Ala
	165	170 175
Asn Asn Glu Asn His Ile Met	Asn Gly Asn Phe Asp Val Ala Ala Ala	
	180	185 190
Pro Tyr Phe Val Ile Gly Ala	Thr Ala Arg Phe Ala Ala Met Gln Ser	
	195	200 205
Tyr Ile Lys Phe Cys Asn Ala Trp	Ile Asp Lys Val Gly Leu Ser Asp	
	210	215 220
Ala Gln Leu Thr Thr Gln Lys Ala Asn Leu	Asp Arg Thr Lys Gln Asn	
	225	230 235 240
Met Arg Asn Ala Ile Leu Asn Tyr Thr	Gln Gln Val Met Lys Val Phe	
	245	250 255
Lys Asp Ser Lys Asn Met Pro Thr	Ile Gly Thr Asn Lys Phe Ser Val	
	260	265 270
Asp Thr Tyr Asn Val Tyr Ile Lys	Gly Met Thr Leu Asn Val Leu Asp	
	275	280 285
Ile Val Ala Ile Trp Pro Ser Leu Tyr Pro	Asp Asp Tyr Thr Ser Gln	
	290	295 300
Thr Ala Leu Glu Gln Thr Arg Val Thr Phe	Ser Asn Met Val Gly Gln	
	305	310 315 320
Glu Glu Gly Thr Asp Gly Ser Leu Arg	Ile Tyr Asn Thr Phe Asp Ser	
	325	330 335
Phe Ser Tyr Gln His Ser Pro Ile	Pro Asn Asn Asn Val Asn Leu Ile	
	340	345 350
Ser Tyr Tyr Asn Asp Glu Leu Gln	Asn Leu Glu Leu Gly Val Tyr Thr	
	355	360 365
Pro Pro Lys Lys Gly Ser Gly Tyr Ser Tyr	Pro Tyr Gly Phe Val Leu	
	370	375 380
Asn Tyr Ala Asn Ser Lys Tyr Lys Tyr	Gly Asp Ser Asn Asp Pro Glu	
	385	390 395 400
Ser Leu Gly Gly Leu Ser Thr Leu Ser	Ala Pro Ile Gln Gln Val Asn	
	405	410 415
Ala Ala Thr Gln Asn Ser Lys Tyr Leu	Asp Gly Glu Ile Leu Asn Gly	
	420	425 430
Ile Gly Ala Ser Leu Pro Gly Tyr Cys	Thr Thr Gly Cys Ser Pro Thr	
	435	440 445
Glu Pro Pro Phe Ser Cys Thr Ser Thr	Ala Asn Gly Tyr Lys Ala Ser	
	450	455 460
Cys Asn Pro Ser Asp Thr Asn Gln Lys	Ile Asn Ala Leu Tyr Pro Phe	
	465	470 475 480
Thr Gln Ala Asn Val Lys Gly Asn Thr	Gly Lys Leu Gly Val Leu Ala	
	485	490 495
Ser Leu Val Ser Tyr Asp Leu Asn Pro	Lys Asn Val Phe Gly Glu Leu	
	500	505 510
Asp Ser Asp Thr Asn Asn Val Ile Leu	Lys Gly Ile Pro Ala Glu Lys	
	515	520 525
Gly Tyr Phe Pro Asn Asn Ala Arg Pro	Thr Val Val Lys Glu Trp Ile	
	530	535 540

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Asn	Gly	Ala	Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met
545					550					555					560
Thr	Ala	Thr	Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr
			565						570					575	
Ala	Asn	Pro	Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn
			580					585					590		
Gly	Ser	Leu	Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp
	595						600					605			
Met	Asn	Asn	Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly
	610					615					620				
Asn	Tyr	Thr	Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr
625				630						635					640
Gly	Asp	Ile	Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile
			645					650						655	
Asp	Arg	Ile	Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn		
		660						665					670		

<210> SEQ ID NO 24

<211> LENGTH: 2174

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: axmi-031(B-D)

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)...(2171)

<400> SEQUENCE: 24

atg gca ata cca gta tct aat gtt aat tcg ttg act gat aca gtt gga	48
Met Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly	
1 5 10 15	
gat tta aaa aaa gca tgg gaa gaa ttt caa aaa act ggt tct ttt tca	96
Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser	
20 25 30	
tta aca gct tta caa caa gga ttt tct gct tca caa gga gga aca ttc	144
Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe	
35 40 45	
aat tat tta aca tta cta caa tca gga ata tca tta gct ggt tct ttt	192
Asn Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe	
50 55 60	
gtt cct gga ggt act ttt gta gca cct att att aat atg gtt att ggt	240
Val Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly	
65 70 75 80	
tggtta tggcca cataaa aacaaa aatgcg gat aca gaa aat tta ata	288
Trp Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile	
85 90 95	
aat tta att gat tca gaa att caa aaa caa tta aac aaa gct tta tta	336
Asn Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu	
100 105 110	
gat gca gat aga aat gag tgg agc tct tat tta gaa tct ata ttt gat	384
Asp Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp	
115 120 125	
tct tca aat aac cta aat ggt gca att gta gat gca cag tgg tca ggc	432
Ser Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly	
130 135 140	
act gta aat act aca aat aga aca cta aga aat cca aca gaa tca gat	480
Thr Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp	
145 150 155 160	

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tat aca aat gtt gtt aca aat ttt att gca gcg gat ggt gac att gca Tyr Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala 165 170 175	528
aat aat gaa aat cac ata atg aat ggc aac ttt gac gta gct gca gca Asn Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala 180 185 190	576
cct tat ttt gtt ata gga gca aca gca cgt ttt gca gca atg caa tct Pro Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser 195 200 205	624
tat att aaa ttt tgt aat gct tgg att gat aaa gtt gga ttg agt gac Tyr Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp 210 215 220	672
gca cag ctt act aca caa aag gct aat tta gat cgc acg aaa caa aat Ala Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn 225 230 235 240	720
atg cgt aat gca att ctt aac tat aca caa caa gtt atg aaa gtt ttt Met Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe 245 250 255	768
aaa gat tcc aaa aat atg cct aca ata ggt act aat aaa ttt agt gtt Lys Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val 260 265 270	816
gat acc tat aat gta tat att aaa gga atg aca tta aat gtt tta gat Asp Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp 275 280 285	864
att gta gca ata tgg cct tca tta tat cca gat gat tat act tca caa Ile Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln 290 295 300	912
aca gcc tta gaa caa aca cgt gtc act ttt tca aat atg gtt ggc caa Thr Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln 305 310 315 320	960
gaa gaa ggt aca gat gga agc cta aga att tac aat act ttt gat tct Glu Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser 325 330 335	1008
ttt agt tat caa cat agt cca ata cct aat aat aat gtt aat tta att Phe Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile 340 345 350	1056
tct tat tat aat gat gaa tta caa aat cta gaa tta gga gta tat acc Ser Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr 355 360 365	1104
cct cct aaa aaa gga agt gga tac tct tat cct tat gga ttt gtt tta Pro Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu 370 375 380	1152
aat tat gca aac agt aaa tat aaa tat ggt gat agc aat gat cca gaa Asn Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu 385 390 395 400	1200
tct cta gga gga tta tct aca cta tct gca cct ata caa caa gtt aat Ser Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn 405 410 415	1248
gca gca act caa aac agt aaa tat cta gat gga gaa atc cta aat gga Ala Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly 420 425 430	1296
ata gga gca tcc tta cct ggt tat tgt act aca gga tgt tca cca aca Ile Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr 435 440 445	1344
gaa cca cct ttt agt tgt act tct acc gct aat ggc tat aaa gca agc Glu Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser 450 455 460	1392

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tgt aat cct tca gat aca aat caa aaa att aac gct tta tat cct ttt Cys Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe 465 470 475 480	1440
aca caa gct aat gta aag gga aac aca gga aaa tta gga gta ctg gca Thr Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala 485 490 495	1488
agt ctt gtt tca tat gat tta aat cct aaa aat gta ttt ggt gaa tta Ser Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu 500 505 510	1536
gat tca gat aca aat aat gtt atc tta aaa gga att cct gca gaa aaa Asp Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys 515 520 525	1584
gga tat ttt cct aat aat gcg cgt cct act gtt gta aaa gaa tgg att Gly Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile 530 535 540	1632
aat ggt gca agt gct gta cca ctt gat tca gga aat acc tta ttt atg Asn Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met 545 550 555 560	1680
acg gct acg aat tta aca gct act caa tat aga att aga ata cgt tat Thr Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr 565 570 575	1728
gca aat cca aat tca aat act caa atc ggt gta cga att aca caa aat Ala Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn 580 585 590	1776
ggt tct cta att tcc agt agt aat cta aca ctt tat agt act act gat Gly Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp 595 600 605	1824
atg aat aat act tta cca cta aat gta tat gta ata gga gaa aat gga Met Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly 610 615 620	1872
aat tat aca ctt caa gat tta tat aat act act aat gtt tta tca aca Asn Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr 625 630 635 640	1920
gga gat att aca tta caa att aca gga gga gat caa aaa ata ttt att Gly Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile 645 650 655	1968
gat cga ata gaa ttt gtt cct act atg cct gta cct ggt aat act aac Asp Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn 660 665 670	2016
aac aat aac ggt aat aat aac ggt aat aat aat ccc cca cac cac gtt Asn Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val 675 680 685	2064
tgt gca ata gct ggt aca caa caa tct tgt tct gga ccg ccc aaa ttt Cys Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe 690 695 700	2112
gaa caa gta agt gat tta gaa aaa att aca aca caa gta tat atg tta Glu Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu 705 710 715 720	2160
ttc aaa tct ta tag Phe Lys Ser	2174

<210> SEQ ID NO 25

<211> LENGTH: 723

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: AXMI-031(B-D)

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<400> SEQUENCE: 25

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Met Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly
 1           5           10           15

Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser
      20           25           30

Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe
      35           40           45

Asn Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe
      50           55           60

Val Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly
      65           70           75           80

Trp Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile
      85           90           95

Asn Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu
      100          105          110

Asp Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp
      115          120          125

Ser Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly
      130          135          140

Thr Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp
      145          150          155          160

Tyr Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala
      165          170          175

Asn Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala
      180          185          190

Pro Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser
      195          200          205

Tyr Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp
      210          215          220

Ala Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn
      225          230          235          240

Met Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe
      245          250          255

Lys Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val
      260          265          270

Asp Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp
      275          280          285

Ile Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln
      290          295          300

Thr Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln
      305          310          315          320

Glu Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser
      325          330          335

Phe Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile
      340          345          350

Ser Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr
      355          360          365

Pro Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu
      370          375          380

Asn Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu
      385          390          395          400

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Ser Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn
 405 410 415
 Ala Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly
 420 425 430
 Ile Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr
 435 440 445
 Glu Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser
 450 455 460
 Cys Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe
 465 470 475 480
 Thr Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala
 485 490 495
 Ser Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu
 500 505 510
 Asp Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys
 515 520 525
 Gly Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile
 530 535 540
 Asn Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met
 545 550 555 560
 Thr Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr
 565 570 575
 Ala Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn
 580 585 590
 Gly Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp
 595 600 605
 Met Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly
 610 615 620
 Asn Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr
 625 630 635 640
 Gly Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile
 645 650 655
 Asp Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn
 660 665 670
 Asn Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val
 675 680 685
 Cys Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe
 690 695 700
 Glu Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu
 705 710 715 720
 Phe Lys Ser

<210> SEQ ID NO 26
 <211> LENGTH: 2226
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synaxmi-031(A-D)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(2226)
 <400> SEQUENCE: 26

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atg cag atc ctt gat tgc aat ctc cag agc cag cag aat atc cca tac	48
Met Gln Ile Leu Asp Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr	
1 5 10 15	
aat gtg ctt gct atc cct gtt agc aat gtt aat agc ctt acg gat acg	96
Asn Val Leu Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr	
20 25 30	
gtt ggc gat cta aag aag gca tgg gaa gag ttc cag aag acg ggc agc	144
Val Gly Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser	
35 40 45	
ttc tcc ctt acc gca ctc cag cag ggc ttc agc gct tcc cag ggc ggg	192
Phe Ser Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly	
50 55 60	
acg ttc aat tac ctc acc ctc ctc cag tcc ggg atc tcc ctg gct ggc	240
Thr Phe Asn Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly	
65 70 75 80	
agc ttc gtg cct ggc ggc acc ttc gtt gct cca atc atc aat atg gtg	288
Ser Phe Val Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val	
85 90 95	
atc ggc tgg ctc tgg cct cat aag aat aag aat gca gat acg gaa aat	336
Ile Gly Trp Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn	
100 105 110	
ctg atc aat ctg atc gat tca gaa atc cag aag cag ctg aat aag gct	384
Leu Ile Asn Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala	
115 120 125	
ctg ctg gat gct gat cgc aat gaa tgg agc agc tac ctc gag tcc atc	432
Leu Leu Asp Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile	
130 135 140	
ttc gat agc agc aat aat ctg aat ggc gca atc gtt gat gct cag tgg	480
Phe Asp Ser Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp	
145 150 155 160	
tcc ggc acc gtg aat acg acc aat cgt acg ctt cgt aat cct acg gaa	528
Ser Gly Thr Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu	
165 170 175	
tca gat tac acc aat gtg gtg acg aat ttc atc gca gca gat ggg gat	576
Ser Asp Tyr Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp	
180 185 190	
atc gct aat aat gaa aat cat atc atg aat ggg aat ttc gat gtg gca	624
Ile Ala Asn Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala	
195 200 205	
gca gct cca tac ttc gtt atc ggg gct acc gct aga ttc gca gct atg	672
Ala Ala Pro Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met	
210 215 220	
cag tcc tac atc aag ttc tgc aat gca tgg atc gat aag gtt ggg ctg	720
Gln Ser Tyr Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu	
225 230 235 240	
tca gat gct cag ctg acc acg cag aag gct aat ctg gat aga acg aag	768
Ser Asp Ala Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys	
245 250 255	
cag aat atg cgt aat gct atc ctt aat tac acc cag cag gtt atg aag	816
Gln Asn Met Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys	
260 265 270	
gtt ttc aag gat tcc aag aat atg cca acg atc ggc acg aat aag ttc	864
Val Phe Lys Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe	
275 280 285	
agc gtt gat acc tac aat gtt tac atc aag ggg atg acg ctt aat gtg	912
Ser Val Asp Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val	
290 295 300	

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ctt gat atc gtt gct atc tgg cca agc ctg tac cca gat gat tac acg	960
Leu Asp Ile Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr	
305 310 315 320	
tca cag acg gct ctg gaa cag acc cgc gtg acg ttc tcc aat atg gtg	1008
Ser Gln Thr Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val	
325 330 335	
ggg cag gaa gaa ggc acg gat ggc agc ctc aga atc tac aat acc ttc	1056
Gly Gln Glu Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe	
340 345 350	
gat agc ttc tcc tac cag cat agc cct atc cct aat aat aat gtg aat	1104
Asp Ser Phe Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn	
355 360 365	
ctc atc agc tac tac aat gat gaa ctt cag aat ctg gaa ctc ggg gtt	1152
Leu Ile Ser Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val	
370 375 380	
tac acc cca cca aag aag ggc tca ggc tac agc tac cca tac ggg ttc	1200
Tyr Thr Pro Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe	
385 390 395 400	
gtg ctg aat tac gca aat agc aag tac aag tac ggc gat tcc aat gat	1248
Val Leu Asn Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp	
405 410 415	
cca gaa tcc ctc ggc ggg ctt tcc acc ctt agc gct cca atc caa cag	1296
Pro Glu Ser Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln	
420 425 430	
gtt aat gct gct acc cag aat agc aag tac ctt gat ggc gaa atc ctg	1344
Val Asn Ala Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu	
435 440 445	
aat ggg atc ggc gca agc ctg cct ggc tac tgc acg acc ggg tgc tca	1392
Asn Gly Ile Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser	
450 455 460	
cct acc gaa cca cca ttc agc tgc acg agc acg gca aat ggg tac aag	1440
Pro Thr Glu Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys	
465 470 475 480	
gca agc tgc aat cca agc gat acc aat cag aag atc aat gct ctc tac	1488
Ala Ser Cys Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr	
485 490 495	
cca ttc acg cag gca aat gtg aag ggg aat acc ggg aag ctg ggc gtt	1536
Pro Phe Thr Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val	
500 505 510	
ctc gca agc ctt gtt agc tac gat ctg aat cct aag aat gtt ttc ggg	1584
Leu Ala Ser Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly	
515 520 525	
gaa ctc gat tca gat acc aat aat gtt atc ctt aag ggc atc cca gca	1632
Glu Leu Asp Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala	
530 535 540	
gaa aag ggc tac ttc cca aat aat gca aga cca acc gtt gtg aag gaa	1680
Glu Lys Gly Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu	
545 550 555 560	
tgg atc aat ggg gct tcc gca gtt cca ctt gat tcc ggc aat acc ctg	1728
Trp Ile Asn Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu	
565 570 575	
ttc atg acg gct acg aac ctg acg gct acc cag tac aga atc cgc atc	1776
Phe Met Thr Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile	
580 585 590	
cgt tac gct aac cca aac tca aac acg cag atc ggc gtt aga atc acg	1824
Arg Tyr Ala Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr	
595 600 605	

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cag aac ggg agc ctc atc tcc tcc tcc aac ctc acg ctg tac tca acc	1872
Gln Asn Gly Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr	
610 615 620	
acc gat atg aac aac acc ctg cca ctg aac gtt tac gtg atc ggg gaa	1920
Thr Asp Met Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu	
625 630 635 640	
aac ggg aac tac acc ctc cag gat ctc tac aac acg acg aac gtt ctg	1968
Asn Gly Asn Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu	
645 650 655	
tcc acg ggc gat atc acc ctg cag atc acc ggc ggg gat cag aag ata	2016
Ser Thr Gly Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile	
660 665 670	
ttc atc gat cgc atc gag ttc gtg cct acg atg cca gtg cca ggc aac	2064
Phe Ile Asp Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn	
675 680 685	
acc aac aac aac aac ggc aac aac aac ggc aac aac aac ccc ccc cat	2112
Thr Asn Asn Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His	
690 695 700	
cat gtc tgc gct ata gct ggt act cag cag tct tgc tca ggt cct cct	2160
His Val Cys Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro	
705 710 715 720	
aag ttc gag cag gtt tct gat ctc gag aag atc acc acc cag gtc tac	2208
Lys Phe Glu Gln Val Ser Asp Leu Lys Ile Thr Thr Gln Val Tyr	
725 730 735	
atg ctg ttc aag tcc taa	2226
Met Leu Phe Lys Ser *	
740	

<210> SEQ ID NO 27

<211> LENGTH: 741

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: SYNAXMI-031(A-D)

<400> SEQUENCE: 27

Met Gln Ile Leu Asp Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr	
1 5 10 15	
Asn Val Leu Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr	
20 25 30	
Val Gly Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser	
35 40 45	
Phe Ser Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly	
50 55 60	
Thr Phe Asn Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly	
65 70 75 80	
Ser Phe Val Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val	
85 90 95	
Ile Gly Trp Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn	
100 105 110	
Leu Ile Asn Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala	
115 120 125	
Leu Leu Asp Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile	
130 135 140	
Phe Asp Ser Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp	
145 150 155 160	
Ser Gly Thr Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu	

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165							170					175			
Ser	Asp	Tyr	Thr	Asn	Val	Val	Thr	Asn	Phe	Ile	Ala	Ala	Asp	Gly	Asp
180							185					190			
Ile	Ala	Asn	Asn	Glu	Asn	His	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala
195							200					205			
Ala	Ala	Pro	Tyr	Phe	Val	Ile	Gly	Ala	Thr	Ala	Arg	Phe	Ala	Ala	Met
210							215					220			
Gln	Ser	Tyr	Ile	Lys	Phe	Cys	Asn	Ala	Trp	Ile	Asp	Lys	Val	Gly	Leu
225							230					235			
Ser	Asp	Ala	Gln	Leu	Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys
245							250					255			
Gln	Asn	Met	Arg	Asn	Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys
260							265					270			
Val	Phe	Lys	Asp	Ser	Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe
275							280					285			
Ser	Val	Asp	Thr	Tyr	Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val
290							295					300			
Leu	Asp	Ile	Val	Ala	Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr
305							310					315			
Ser	Gln	Thr	Ala	Leu	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val
325							330					335			
Gly	Gln	Glu	Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe
340							345					350			
Asp	Ser	Phe	Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Val	Asn	
355							360					365			
Leu	Ile	Ser	Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val
370							375					380			
Tyr	Thr	Pro	Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe
385							390					395			
Val	Leu	Asn	Tyr	Ala	Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp
405							410					415			
Pro	Glu	Ser	Leu	Gly	Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln
420							425					430			
Val	Asn	Ala	Ala	Thr	Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu
435							440					445			
Asn	Gly	Ile	Gly	Ala	Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser
450							455					460			
Pro	Thr	Glu	Pro	Pro	Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys
465							470					475			
Ala	Ser	Cys	Asn	Pro	Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr
485							490					495			
Pro	Phe	Thr	Gln	Ala	Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val
500							505					510			
Leu	Ala	Ser	Leu	Val	Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly
515							520					525			
Glu	Leu	Asp	Ser	Asp	Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala
530							535					540			
Glu	Lys	Gly	Tyr	Phe	Pro	Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu
545							550					555			
Trp	Ile	Asn	Gly	Ala	Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu
565							570					575			

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Phe Met Thr Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile
 580 585 590
 Arg Tyr Ala Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr
 595 600 605
 Gln Asn Gly Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr
 610 615 620
 Thr Asp Met Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu
 625 630 635 640
 Asn Gly Asn Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu
 645 650 655
 Ser Thr Gly Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile
 660 665 670
 Phe Ile Asp Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn
 675 680 685
 Thr Asn Asn Asn Asn Gly Asn Asn Asn Gly Asn Asn Pro Pro His
 690 695 700
 His Val Cys Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro
 705 710 715 720
 Lys Phe Glu Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr
 725 730 735
 Met Leu Phe Lys Ser
 740

<210> SEQ ID NO 28
 <211> LENGTH: 2316
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: aposynaxmi-031(A-D)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(2316)

<400> SEQUENCE: 28

atg cag atc ctt ggg tac tcc agc ttc gtt gct atc gct ctt ctt atg	48
Met Gln Ile Leu Gly Tyr Ser Ser Phe Val Ala Ile Ala Leu Leu Met	
1 5 10 15	
agc gtg gtt gtt gtt tgc aat ggg ggc aag acg tcc acc tac gtg cgt	96
Ser Val Val Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg	
20 25 30	
aat ctg gat tgc aat ctc cag agc cag cag aat atc cca tac aat gtg	144
Asn Leu Asp Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val	
35 40 45	
ctt gct atc cct gtt agc aat gtt aat agc ctt acg gat acg gtt ggc	192
Leu Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly	
50 55 60	
gat cta aag aag gca tgg gaa gag ttc cag aag acg ggc agc ttc tcc	240
Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser	
65 70 75 80	
ctt acc gca ctc cag cag ggc ttc agc gct tcc cag ggc ggc acg ttc	288
Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe	
85 90 95	
aat tac ctc acc ctc ctc cag tcc ggg atc tcc ctg gct ggc agc ttc	336
Asn Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe	
100 105 110	
gtg cct ggc ggc acc ttc gtt gct cca atc atc aat atg gtg atc ggc	384

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Val	Pro	Gly	Gly	Thr	Phe	Val	Ala	Pro	Ile	Ile	Asn	Met	Val	Ile	Gly	
		115					120					125				
tgg	ctc	tgg	cct	cat	aag	aat	aag	aat	gca	gat	acg	gaa	aat	ctg	atc	432
Trp	Leu	Trp	Pro	His	Lys	Asn	Lys	Asn	Ala	Asp	Thr	Glu	Asn	Leu	Ile	
	130					135					140					
aat	ctg	atc	gat	tca	gaa	atc	cag	aag	cag	ctg	aat	aag	gct	ctg	ctg	480
Asn	Leu	Ile	Asp	Ser	Glu	Ile	Gln	Lys	Gln	Leu	Asn	Lys	Ala	Leu	Leu	
	145				150					155					160	
gat	gct	gat	cgc	aat	gaa	tgg	agc	agc	tac	ctc	gag	tcc	atc	ttc	gat	528
Asp	Ala	Asp	Arg	Asn	Glu	Trp	Ser	Ser	Tyr	Leu	Glu	Ser	Ile	Phe	Asp	
				165					170					175		
agc	agc	aat	aat	ctg	aat	ggc	gca	atc	gtt	gat	gct	cag	tgg	tcc	ggc	576
Ser	Ser	Asn	Asn	Leu	Asn	Gly	Ala	Ile	Val	Asp	Ala	Gln	Trp	Ser	Gly	
		180						185					190			
acc	gtg	aat	acg	acc	aat	cgt	acg	ctt	cgt	aat	cct	acg	gaa	tca	gat	624
Thr	Val	Asn	Thr	Thr	Asn	Arg	Thr	Leu	Arg	Asn	Pro	Thr	Glu	Ser	Asp	
		195					200					205				
tac	acc	aat	gtg	gtg	acg	aat	ttc	atc	gca	gca	gat	ggg	gat	atc	gct	672
Tyr	Thr	Asn	Val	Val	Thr	Asn	Phe	Ile	Ala	Ala	Asp	Gly	Asp	Ile	Ala	
	210					215					220					
aat	aat	gaa	aat	cat	atc	atg	aat	ggg	aat	ttc	gat	gtg	gca	gca	gct	720
Asn	Asn	Glu	Asn	His	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala	Ala	Ala	
	225				230				235						240	
cca	tac	ttc	gtt	atc	ggg	gct	acc	gct	aga	ttc	gca	gct	atg	cag	tcc	768
Pro	Tyr	Phe	Val	Ile	Gly	Ala	Thr	Ala	Arg	Phe	Ala	Ala	Met	Gln	Ser	
			245						250					255		
tac	atc	aag	ttc	tgc	aat	gca	tgg	atc	gat	aag	gtt	ggg	ctg	tca	gat	816
Tyr	Ile	Lys	Phe	Cys	Asn	Ala	Trp	Ile	Asp	Lys	Val	Gly	Leu	Ser	Asp	
		260					265						270			
gct	cag	ctg	acc	acg	cag	aag	gct	aat	ctg	gat	aga	acg	aag	cag	aat	864
Ala	Gln	Leu	Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys	Gln	Asn	
		275					280					285				
atg	cgt	aat	gct	atc	ctt	aat	tac	acc	cag	cag	gtt	atg	aag	gtt	ttc	912
Met	Arg	Asn	Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys	Val	Phe	
		290				295					300					
aag	gat	tcc	aag	aat	atg	cca	acg	atc	ggc	acg	aat	aag	ttc	agc	gtt	960
Lys	Asp	Ser	Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val	
	305				310				315						320	
gat	acc	tac	aat	gtt	tac	atc	aag	ggg	atg	acg	ctt	aat	gtg	ctt	gat	1008
Asp	Thr	Tyr	Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	
			325						330					335		
atc	gtt	gct	atc	tgg	cca	agc	ctg	tac	cca	gat	gat	tac	acg	tca	cag	1056
Ile	Val	Ala	Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr	Ser	Gln	
			340					345						350		
acg	gct	ctg	gaa	cag	acc	cgc	gtg	acg	ttc	tcc	aat	atg	gtg	ggg	cag	1104
Thr	Ala	Leu	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	
		355					360					365				
gaa	gaa	ggc	acg	gat	ggc	agc	ctc	aga	atc	tac	aat	acc	ttc	gat	agc	1152
Glu	Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	
		370				375					380					
ttc	tcc	tac	cag	cat	agc	cct	atc	cct	aat	aat	aat	gtg	aat	ctc	atc	1200
Phe	Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	
					390					395					400	
agc	tac	tac	aat	gat	gaa	ctt	cag	aat	ctg	gaa	ctc	ggg	gtt	tac	acc	1248
Ser	Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	
				405					410					415		
cca	cca	aag	aag	ggc	tca	ggc	tac	agc	tac	cca	tac	ggg	ttc	gtg	ctg	1296

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Pro	Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	
			420					425					430			
aat	tac	gca	aat	agc	aag	tac	aag	tac	ggc	gat	tcc	aat	gat	cca	gaa	1344
Asn	Tyr	Ala	Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu	
		435					440					445				
tcc	ctc	ggc	ggg	ctt	tcc	acc	ctt	agc	gct	cca	atc	caa	cag	gtt	aat	1392
Ser	Leu	Gly	Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn	
	450						455				460					
gct	gct	acc	cag	aat	agc	aag	tac	ctt	gat	ggc	gaa	atc	ctg	aat	ggg	1440
Ala	Ala	Thr	Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu	Asn	Gly	
465						470				475					480	
atc	ggc	gca	agc	ctg	cct	ggc	tac	tgc	acg	acc	ggg	tgc	tca	cct	acc	1488
Ile	Gly	Ala	Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr	
			485						490					495		
gaa	cca	cca	ttc	agc	tgc	acg	agc	acg	gca	aat	ggg	tac	aag	gca	agc	1536
Glu	Pro	Pro	Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser	
			500					505					510			
tgc	aat	cca	agc	gat	acc	aat	cag	aag	atc	aat	gct	ctc	tac	cca	ttc	1584
Cys	Asn	Pro	Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe	
		515					520					525				
acg	cag	gca	aat	gtg	aag	ggg	aat	acc	ggg	aag	ctg	ggc	gtt	ctc	gca	1632
Thr	Gln	Ala	Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	
	530					535					540					
agc	ctt	gtt	agc	tac	gat	ctg	aat	cct	aag	aat	gtt	ttc	ggg	gaa	ctc	1680
Ser	Leu	Val	Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu	
	545					550				555					560	
gat	tca	gat	acc	aat	aat	gtt	atc	ctt	aag	ggc	atc	cca	gca	gaa	aag	1728
Asp	Ser	Asp	Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys	
			565					570					575			
ggc	tac	ttc	cca	aat	aat	gca	aga	cca	acc	gtt	gtg	aag	gaa	tgg	atc	1776
Gly	Tyr	Phe	Pro	Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu	Trp	Ile	
			580					585					590			
aat	ggg	gct	tcc	gca	gtt	cca	ctt	gat	tcc	ggc	aat	acc	ctg	ttc	atg	1824
Asn	Gly	Ala	Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met	
		595					600					605				
acg	gct	acg	aac	ctg	acg	gct	acc	cag	tac	aga	atc	cgc	atc	cgt	tac	1872
Thr	Ala	Thr	Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr	
	610					615					620					
gct	aac	cca	aac	tca	aac	acg	cag	atc	ggc	gtt	aga	atc	acg	cag	aac	1920
Ala	Asn	Pro	Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn	
	625					630				635					640	
ggg	agc	ctc	atc	tcc	tcc	tcc	aac	ctc	acg	ctg	tac	tca	acc	acc	gat	1968
Gly	Ser	Leu	Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp	
			645						650					655		
atg	aac	aac	acc	ctg	cca	ctg	aac	gtt	tac	gtg	atc	ggg	gaa	aac	ggg	2016
Met	Asn	Asn	Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly	
			660					665					670			
aac	tac	acc	ctc	cag	gat	ctc	tac	aac	acg	acg	aac	gtt	ctg	tcc	acg	2064
Asn	Tyr	Thr	Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr	
		675					680					685				
ggc	gat	atc	acc	ctg	cag	atc	acc	ggc	ggg	gat	cag	aag	ata	ttc	atc	2112
Gly	Asp	Ile	Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile	
	690					695					700					
gat	cgc	atc	gag	ttc	gtg	cct	acg	atg	cca	gtg	cca	ggc	aac	acc	aac	2160
Asp	Arg	Ile	Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn	Thr	Asn	
	705				710					715					720	
aac	aac	aac	ggc	aac	aac	aac	ggc	aac	aac	aac	ccc	ccc	cat	cat	gtc	2208

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Asn	Asn	Asn	Gly	Asn	Asn	Asn	Gly	Asn	Asn	Asn	Pro	Pro	His	His	Val	
			725						730					735		
tgc	gct	ata	gct	ggg	act	cag	cag	tct	tgc	tca	ggg	cct	cct	aag	ttc	2256
Cys	Ala	Ile	Ala	Gly	Thr	Gln	Gln	Ser	Cys	Ser	Gly	Pro	Pro	Lys	Phe	
			740						745					750		
gag	cag	gtt	tct	gat	ctc	gag	aag	atc	acc	acc	cag	gtc	tac	atg	ctg	2304
Glu	Gln	Val	Ser	Asp	Leu	Glu	Lys	Ile	Thr	Thr	Gln	Val	Tyr	Met	Leu	
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Phe	Lys	Ser	*													
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<210> SEQ ID NO 29

<211> LENGTH: 771

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: APOSYNAXMI-031(A-D)

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			20					25					30			
Asn	Leu	Asp	Cys	Asn	Leu	Gln	Ser	Gln	Gln	Asn	Ile	Pro	Tyr	Asn	Val	
		35				40						45				
Leu	Ala	Ile	Pro	Val	Ser	Asn	Val	Asn	Ser	Leu	Thr	Asp	Thr	Val	Gly	
	50				55					60						
Asp	Leu	Lys	Lys	Ala	Trp	Glu	Glu	Phe	Gln	Lys	Thr	Gly	Ser	Phe	Ser	
65				70					75					80		
Leu	Thr	Ala	Leu	Gln	Gly	Phe	Ser	Ala	Ser	Gln	Gly	Gly	Thr	Phe		
			85					90					95			
Asn	Tyr	Leu	Thr	Leu	Leu	Gln	Ser	Gly	Ile	Ser	Leu	Ala	Gly	Ser	Phe	
		100						105					110			
Val	Pro	Gly	Gly	Thr	Phe	Val	Ala	Pro	Ile	Ile	Asn	Met	Val	Ile	Gly	
	115					120						125				
Trp	Leu	Trp	Pro	His	Lys	Asn	Lys	Asn	Ala	Asp	Thr	Glu	Asn	Leu	Ile	
	130				135					140						
Asn	Leu	Ile	Asp	Ser	Glu	Ile	Gln	Lys	Gln	Leu	Asn	Lys	Ala	Leu	Leu	
145				150						155				160		
Asp	Ala	Asp	Arg	Asn	Glu	Trp	Ser	Ser	Tyr	Leu	Glu	Ser	Ile	Phe	Asp	
			165						170					175		
Ser	Ser	Asn	Asn	Leu	Asn	Gly	Ala	Ile	Val	Asp	Ala	Gln	Trp	Ser	Gly	
		180						185					190			
Thr	Val	Asn	Thr	Thr	Asn	Arg	Thr	Leu	Arg	Asn	Pro	Thr	Glu	Ser	Asp	
	195					200						205				
Tyr	Thr	Asn	Val	Val	Thr	Asn	Phe	Ile	Ala	Ala	Asp	Gly	Asp	Ile	Ala	
	210					215					220					
Asn	Asn	Glu	Asn	His	Ile	Met	Asn	Gly	Asn	Phe	Asp	Val	Ala	Ala	Ala	
225				230						235				240		
Pro	Tyr	Phe	Val	Ile	Gly	Ala	Thr	Ala	Arg	Phe	Ala	Ala	Met	Gln	Ser	
			245					250						255		
Tyr	Ile	Lys	Phe	Cys	Asn	Ala	Trp	Ile	Asp	Lys	Val	Gly	Leu	Ser	Asp	
		260						265					270			

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Ala	Gln	Leu	Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys	Gln	Asn
	275						280					285			
Met	Arg	Asn	Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys	Val	Phe
	290					295					300				
Lys	Asp	Ser	Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val
305					310					315					320
Asp	Thr	Tyr	Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp
				325					330					335	
Ile	Val	Ala	Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr	Ser	Gln
		340						345					350		
Thr	Ala	Leu	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln
	355						360					365			
Glu	Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser
	370					375					380				
Phe	Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile
385					390					395					400
Ser	Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr
			405						410					415	
Pro	Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu
		420						425					430		
Asn	Tyr	Ala	Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu
		435					440					445			
Ser	Leu	Gly	Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn
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Ile	Gly	Ala	Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr
			485					490						495	
Glu	Pro	Pro	Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser
		500					505						510		
Cys	Asn	Pro	Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe
	515						520					525			
Thr	Gln	Ala	Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala
	530					535					540				
Ser	Leu	Val	Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu
545					550					555					560
Asp	Ser	Asp	Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys
			565						570					575	
Gly	Tyr	Phe	Pro	Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu	Trp	Ile
		580						585					590		
Asn	Gly	Ala	Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met
	595						600					605			
Thr	Ala	Thr	Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr
	610					615					620				
Ala	Asn	Pro	Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn
625						630				635					640
Gly	Ser	Leu	Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp
			645						650					655	
Met	Asn	Asn	Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly
		660						665					670		
Asn	Tyr	Thr	Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr

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675	680	685	
Gly Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile			
690	695	700	
Asp Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn			
705	710	715	720
Asn Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val			
	725	730	735
Cys Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe			
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Glu Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu			
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Phe Lys Ser			
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1 5 10 15			
gtg gtg tgc aac ggc ggc aag aca agc acc tat gtg agg aac ctg gac			96
Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg Asn Leu Asp			
20 25 30			
tgc aac ctg cag agc cag cag aac atc ccc tac aat gtg ctg gcc atc			144
Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu Ala Ile			
35 40 45			
ccc gtc tca aat gtc aac agc ttg aca gat act gtt ggt gat ttg aag			192
Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp Leu Lys			
50 55 60			
aag gca tgg gag gag ttc cag aag acc ggc agc ttc agc ttg acg gcg			240
Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu Thr Ala			
65 70 75 80			
ctg caa caa ggc ttc tca gca agc caa gga ggc acc ttc aac tac ctg			288
Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn Tyr Leu			
85 90 95			
acc ttg ctg caa agc ggc atc agc ttg gcc ggc agc ttc gtg ccc ggc			336
Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val Pro Gly			
100 105 110			
ggc acc ttc gtg gcg ccc atc atc aac atg gtg att gga tgg ctg tgg			384
Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp Leu Trp			
115 120 125			
ccg cac aag aac aag aat gct gac aca gaa aat ttg atc aac ctg att			432
Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn Leu Ile			
130 135 140			
gat tca gag atc cag aag cag ctg aac aag gcg ctg ctg gat gct gac			480
Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp Ala Asp			
145 150 155 160			
aga aat gaa tgg agc agc tac ctg gag agc atc ttt gat tca agc aac			528
Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser Ser Asn			
165 170 175			

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gtg gtg acc aac ttc att gct gct gat gga gac atc gcc aac aat gag Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn Asn Glu 210 215 220	672
aac cac atc atg aat gga aat ttt gat gtt gct gct gct cca tat ttt Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Pro Tyr Phe 225 230 235 240	720
gtg att gga gca aca gca aga ttt gct gcc atg caa tca tac atc aag Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr Ile Lys 245 250 255	768
ttc tgc aat gca tgg atc gac aag gtg ggc ctc tct gat gct cag ctc Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala Gln Leu 260 265 270	816
acc acc cag aag gcc aac ctg gac agg acc aag cag aac atg agg aat Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met Arg Asn 275 280 285	864
gcc atc ttg aat tac acc cag cag gtg atg aag gtg ttc aag gac agc Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys Asp Ser 290 295 300	912
aag aac atg cca acc atc ggc acc aac aag ttc tca gtg gac acc tac Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp Thr Tyr 305 310 315 320	960
aat gtc tac atc aag ggc atg acg ctc aat gtg ctg gac atc gtc gcc Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile Val Ala 325 330 335	1008
atc tgg cca agc ctc tac cct gat gac tac acc tca cag acg gcg ctg Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr Ala Leu 340 345 350	1056
gag caa aca agg gtg acc ttc agc aac atg gtg ggc caa gaa gaa gga Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu Glu Gly 355 360 365	1104
act gat ggc agc ttg agg atc tac aac acc ttc gac agc ttc agc tac Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe Ser Tyr 370 375 380	1152
cag cat tct ccc atc ccc aac aac aat gtc aac ctc atc agc tac tac Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser Tyr Tyr 385 390 395 400	1200
aat gat gag ctg caa aat ttg gag cta gga gtc tac acg ccg cca aag Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro Pro Lys 405 410 415	1248
aaa gga agt gga tat tct tat cct tat ggc ttc gtg ctc aac tac gcc Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn Tyr Ala 420 425 430	1296
aac agc aag tac aag tat gga gat tca aat gat cca gaa agc ctc ggc Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser Leu Gly 435 440 445	1344
ggc ctc tcc acc ttg tcg gcg ccc atc cag cag gtg aac gcc gcc acc Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala Ala Thr 450 455 460	1392
cag aac agc aag tac ctt gat gga gag atc ctc aat ggc att gga gct Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile Gly Ala 465 470 475 480	1440

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tct ctt cct ggc tac tgc acc acc ggc tgc tcg ccg acg gag ccg ccc Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu Pro Pro 485 490 495	1488
ttc agc tgc acc tca aca gca aat ggc tac aag gca agc tgc aac ccc Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys Asn Pro 500 505 510	1536
tcc gac acc aac cag aag atc aac gcg ctc tac ccc ttc acc caa gct Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr Gln Ala 515 520 525	1584
aat gtg aag ggc aac acc ggc aag ctc ggc gtg ctg gcc agc ttg gtg Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser Leu Val 530 535 540	1632
agc tac gac ctc aac ccc aag aat gtt ttt gga gag ctg gac agc gac Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp Ser Asp 545 550 555 560	1680
acc aac aat gtc atc cta aag ggc atc ccg gcg gag aag ggc tac ttc Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly Tyr Phe 565 570 575	1728
ccc aac aat gca agg ccg acg gtg gtg aag gag tgg atc aat gga gct Pro Asn Asn Ala Arg Pro Thr Val Lys Glu Trp Ile Asn Gly Ala 580 585 590	1776
tcg gcg gtg cct ctt gat tca ggc aac acc ttg ttc atg aca gca aca Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr Ala Thr 595 600 605	1824
aat ttg acg gcg acg cag tac agg atc agg atc aga tat gcc aac ccc Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala Asn Pro 610 615 620	1872
aac agc aac acc cag atc ggc gtg agg atc acc caa aat gga agc ctc Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly Ser Leu 625 630 635 640	1920
atc agc agc agc aac ctc acc ctc tac tca aca act gac atg aac aac Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met Asn Asn 645 650 655	1968
acc ttg ccg ctc aat gtt tat gtg att gga gaa aat ggc aac tac acc Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn Tyr Thr 660 665 670	2016
ttg caa gat ctc tac aac acc acc aac gtg ctg agc acc ggc gac atc Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly Asp Ile 675 680 685	2064
acc cta cag atc act gga gga gat cag aag atc ttc atc gac agg att Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp Arg Ile 690 695 700	2112
gaa ttt gtt cca aca atg cca gtt cct ggc aac acc aac aac aac aat Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn Asn Asn Asn 705 710 715 720	2160
ggc aac aac aat ggc aac aac aac ccg ccg cac cat gtt tgt gcc ata Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val Cys Ala Ile 725 730 735	2208
gct gga act caa caa agc tgc tct ggg ccg cca aaa ttt gag caa gtt Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe Glu Gln Val 740 745 750	2256
tca gat ctg gag aag atc acc acc caa gtc tac atg ctc ttc aag agc Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu Phe Lys Ser 755 760 765	2304
taa *	2307

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<210> SEQ ID NO 31
<211> LENGTH: 768
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: APOSYN2AXMI-031(A-D)

<400> SEQUENCE: 31

Met Gly Tyr Ser Ser Phe Val Ala Ile Ala Leu Leu Met Ser Val Val
1 5 10 15

Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg Asn Leu Asp
20 25 30

Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu Ala Ile
35 40 45

Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp Leu Lys
50 55 60

Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu Thr Ala
65 70 75 80

Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn Tyr Leu
85 90 95

Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val Pro Gly
100 105 110

Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp Leu Trp
115 120 125

Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn Leu Ile
130 135 140

Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp Ala Asp
145 150 155 160

Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser Ser Asn
165 170 175

Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr Val Asn
180 185 190

Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr Thr Asn
195 200 205

Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn Asn Glu
210 215 220

Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro Tyr Phe
225 230 235 240

Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr Ile Lys
245 250 255

Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala Gln Leu
260 265 270

Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met Arg Asn
275 280 285

Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys Asp Ser
290 295 300

Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp Thr Tyr
305 310 315 320

Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile Val Ala
325 330 335

Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr Ala Leu
340 345 350

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Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	Glu	Glu	Gly
	355						360				365				
Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Phe	Ser	Tyr
	370					375				380					
Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser	Tyr	Tyr
385					390				395						400
Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	Pro	Pro	Lys
			405						410					415	
Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn	Tyr	Ala
		420						425					430		
Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu	Ser	Leu	Gly
		435					440					445			
Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn	Ala	Ala	Thr
	450					455					460				
Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu	Asn	Gly	Ile	Gly	Ala
465					470					475					480
Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr	Glu	Pro	Pro
			485						490					495	
Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser	Cys	Asn	Pro
		500						505					510		
Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe	Thr	Gln	Ala
		515					520					525			
Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	Ser	Leu	Val
	530					535					540				
Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu	Asp	Ser	Asp
545					550					555					560
Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys	Gly	Tyr	Phe
			565						570					575	
Pro	Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu	Trp	Ile	Asn	Gly	Ala
			580					585					590		
Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met	Thr	Ala	Thr
		595					600					605			
Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr	Ala	Asn	Pro
	610					615					620				
Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn	Gly	Ser	Leu
625					630					635					640
Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp	Met	Asn	Asn
				645					650					655	
Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly	Asn	Tyr	Thr
		660						665					670		
Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr	Gly	Asp	Ile
	675						680					685			
Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile	Asp	Arg	Ile
	690					695					700				
Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn	Thr	Asn	Asn	Asn	Asn
705					710					715					720
Gly	Asn	Asn	Asn	Gly	Asn	Asn	Asn	Pro	Pro	His	His	Val	Cys	Ala	Ile
				725					730					735	
Ala	Gly	Thr	Gln	Gln	Ser	Cys	Ser	Gly	Pro	Pro	Lys	Phe	Glu	Gln	Val
		740						745					750		
Ser	Asp	Leu	Glu	Lys	Ile	Thr	Thr	Gln	Val	Tyr	Met	Leu	Phe	Lys	Ser

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755	760	765	
<210> SEQ ID NO 32			
<211> LENGTH: 3570			
<212> TYPE: DNA			
<213> ORGANISM: Artificial Sequence			
<220> FEATURE:			
<223> OTHER INFORMATION: synaxmi-031(fl)-ER			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)...(3570)			
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Met Asp Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu			
1 5 10 15			
gct atc cct gtt agc aat gtt aat agc ctt acg gat acg gtt ggc gat			96
Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp			
20 25 30			
cta aag aag gca tgg gaa gag ttc cag aag acg ggc agc ttc tcc ctt			144
Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu			
35 40 45			
acc gca ctc cag cag ggc ttc agc gct tcc cag ggc ggg acg ttc aat			192
Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn			
50 55 60			
tac ctc acc ctc ctc cag tcc ggg atc tcc ctg gct ggc agc ttc gtg			240
Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val			
65 70 75 80			
cct ggc ggc acc ttc gtt gct cca atc atc aat atg gtg atc ggc tgg			288
Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp			
85 90 95			
ctc tgg cct cat aag aat aag aat gca gat acg gaa aat ctg atc aat			336
Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn			
100 105 110			
ctg atc gat tca gaa atc cag aag cag ctg aat aag gct ctg ctg gat			384
Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp			
115 120 125			
gct gat cgc aat gaa tgg agc agc tac ctc gag tcc atc ttc gat agc			432
Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser			
130 135 140			
agc aat aat ctg aat ggc gca atc gtt gat gct cag tgg tcc ggc acc			480
Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr			
145 150 155 160			
gtg aat acg acc aat cgt acg ctt cgt aat cct acg gaa tca gat tac			528
Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr			
165 170 175			
acc aat gtg gtg acg aat ttc atc gca gca gat ggg gat atc gct aat			576
Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn			
180 185 190			
aat gaa aat cat atc atg aat ggg aat ttc gat gtg gca gca gct cca			624
Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Pro			
195 200 205			
tac ttc gtt atc ggg gct acc gct aga ttc gca gct atg cag tcc tac			672
Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr			
210 215 220			
atc aag ttc tgc aat gca tgg atc gat aag gtt ggg ctg tca gat gct			720
Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala			
225 230 235 240			
cag ctg acc acg cag aag gct aat ctg gat aga acg aag cag aat atg			768

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Gln	Leu	Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys	Gln	Asn	Met	
				245					250					255		
cgt	aat	gct	atc	ctt	aat	tac	acc	cag	cag	gtt	atg	aag	gtt	ttc	aag	816
Arg	Asn	Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys	Val	Phe	Lys	
				260				265					270			
gat	tcc	aag	aat	atg	cca	acg	atc	ggc	acg	aat	aag	ttc	agc	gtt	gat	864
Asp	Ser	Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val	Asp	
		275					280					285				
acc	tac	aat	gtt	tac	atc	aag	ggg	atg	acg	ctt	aat	gtg	ctt	gat	atc	912
Thr	Tyr	Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	Ile	
		290				295					300					
gtt	gct	atc	tgg	cca	agc	ctg	tac	cca	gat	gat	tac	acg	tca	cag	acg	960
Val	Ala	Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr	Ser	Gln	Thr	
305					310				315					320		
gct	ctg	gaa	cag	acc	cgc	gtg	acg	ttc	tcc	aat	atg	gtg	ggg	cag	gaa	1008
Ala	Leu	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	Glu	
			325						330					335		
gaa	ggc	acg	gat	ggc	agc	ctc	aga	atc	tac	aat	acc	ttc	gat	agc	ttc	1056
Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Phe	
			340					345					350			
tcc	tac	cag	cat	agc	cct	atc	cct	aat	aat	aat	gtg	aat	ctc	atc	agc	1104
Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser	
		355					360					365				
tac	tac	aat	gat	gaa	ctt	cag	aat	ctg	gaa	ctc	ggg	gtt	tac	acc	cca	1152
Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	Pro	
		370				375					380					
cca	aag	aag	ggc	tca	ggc	tac	agc	tac	cca	tac	ggg	ttc	gtg	ctg	aat	1200
Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn	
385					390				395					400		
tac	gca	aat	agc	aag	tac	aag	tac	ggc	gat	tcc	aat	gat	cca	gaa	tcc	1248
Tyr	Ala	Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu	Ser	
			405						410					415		
ctc	ggc	ggg	ctt	tcc	acc	ctt	agc	gct	cca	atc	caa	cag	gtt	aat	gct	1296
Leu	Gly	Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn	Ala	
			420					425					430			
gct	acc	cag	aat	agc	aag	tac	ctt	gat	ggc	gaa	atc	ctg	aat	ggg	atc	1344
Ala	Thr	Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu	Asn	Gly	Ile	
		435					440					445				
ggc	gca	agc	ctg	cct	ggc	tac	tgc	acg	acc	ggg	tgc	tca	cct	acc	gaa	1392
Gly	Ala	Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr	Glu	
		450				455					460					
cca	cca	ttc	agc	tgc	acg	agc	acg	gca	aat	ggg	tac	aag	gca	agc	tgc	1440
Pro	Pro	Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser	Cys	
465					470					475				480		
aat	cca	agc	gat	acc	aat	cag	aag	atc	aat	gct	ctc	tac	cca	ttc	acg	1488
Asn	Pro	Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe	Thr	
				485					490					495		
cag	gca	aat	gtg	aag	ggg	aat	acc	ggg	aag	ctg	ggc	gtt	ctc	gca	agc	1536
Gln	Ala	Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala	Ser	
			500					505					510			
ctt	gtt	agc	tac	gat	ctg	aat	cct	aag	aat	gtt	ttc	ggg	gaa	ctc	gat	1584
Leu	Val	Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu	Asp	
			515				520					525				
tca	gat	acc	aat	aat	gtt	atc	ctt	aag	ggc	atc	cca	gca	gaa	aag	ggc	1632
Ser	Asp	Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys	Gly	
		530				535					540					
tac	ttc	cca	aat	aat	gca	aga	cca	acc	gtt	gtg	aag	gaa	tgg	atc	aat	1680

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Tyr 545	Phe	Pro	Asn	Asn	Ala 550	Arg	Pro	Thr	Val	Val 555	Lys	Glu	Trp	Ile	Asn 560	
ggg	gct	tcc	gca	gtt	cca	ctt	gat	tcc	ggc	aat	acc	ctg	ttc	atg	acg	1728
Gly	Ala	Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met	Thr	
			565						570					575		
gct	acg	aac	ctg	acg	gct	acc	cag	tac	aga	atc	cgc	atc	cgt	tac	gct	1776
Ala	Thr	Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr	Ala	
			580					585					590			
aac	cca	aac	tca	aac	acg	cag	atc	ggc	gtt	aga	atc	acg	cag	aac	ggg	1824
Asn	Pro	Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn	Gly	
		595					600					605				
agc	ctc	atc	tcc	tcc	tcc	aac	ctc	acg	ctg	tac	tca	acc	acc	gat	atg	1872
Ser	Leu	Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp	Met	
	610					615					620					
aac	aac	acc	ctg	cca	ctg	aac	gtt	tac	gtg	atc	ggg	gaa	aac	ggg	aac	1920
Asn	Asn	Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly	Asn	
625					630					635					640	
tac	acc	ctc	cag	gat	ctc	tac	aac	acg	acg	aac	gtt	ctg	tcc	acg	ggc	1968
Tyr	Thr	Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr	Gly	
			645						650					655		
gat	atc	acc	ctg	cag	atc	acc	ggc	ggg	gat	cag	aag	ata	ttc	atc	gat	2016
Asp	Ile	Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile	Asp	
			660					665					670			
cgc	atc	gag	ttc	gtg	cct	acg	atg	cca	gtg	cca	ggc	aac	acc	aac	aac	2064
Arg	Ile	Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn	Thr	Asn	Asn	
		675					680					685				
aac	aac	ggg	aac	aac	aac	ggc	aac	aac	aac	cct	cct	cat	cat	gtt	tgc	2112
Asn	Asn	Gly	Asn	Asn	Asn	Gly	Asn	Asn	Asn	Pro	Pro	His	His	Val	Cys	
		690				695						700				
gct	atc	gca	ggc	acc	cag	cag	tcc	tgc	tcc	ggc	cca	cca	aag	ttc	gag	2160
Ala	Ile	Ala	Gly	Thr	Gln	Gln	Ser	Cys	Ser	Gly	Pro	Pro	Lys	Phe	Glu	
705					710					715					720	
cag	gtg	tcc	gat	tta	gaa	aag	ata	acc	acg	cag	gtt	tac	atg	ctc	ttc	2208
Gln	Val	Ser	Asp	Leu	Glu	Lys	Ile	Thr	Thr	Gln	Val	Tyr	Met	Leu	Phe	
			725						730					735		
aag	tcc	tcc	cca	tac	gaa	gaa	ctt	gct	ctt	gaa	gtt	agc	agc	tac	cag	2256
Lys	Ser	Ser	Pro	Tyr	Glu	Glu	Leu	Ala	Leu	Glu	Val	Ser	Ser	Tyr	Gln	
			740					745						750		
atc	agc	cag	gtt	gca	ctg	aag	gtt	atg	gct	ctc	agc	gat	gaa	cta	ttc	2304
Ile	Ser	Gln	Val	Ala	Leu	Lys	Val	Met	Ala	Leu	Ser	Asp	Glu	Leu	Phe	
		755					760						765			
tgc	gaa	gaa	aag	aac	gtg	ctg	aga	aag	ctc	gtg	aac	aag	gca	aag	cag	2352
Cys	Glu	Glu	Lys	Asn	Val	Leu	Arg	Lys	Leu	Val	Asn	Lys	Ala	Lys	Gln	
		770					775					780				
ctt	ctc	gaa	gca	agc	aac	ctt	ctc	gtt	ggg	ggg	aac	ttc	gag	acg	act	2400
Leu	Leu	Glu	Ala	Ser	Asn	Leu	Leu	Val	Gly	Gly	Asn	Phe	Glu	Thr	Thr	
					790					795					800	
cag	aac	tgg	gtg	ctc	ggc	acg	aac	gct	tac	atc	aac	tat	gat	tca	ttc	2448
Gln	Asn	Trp	Val	Leu	Gly	Thr	Asn	Ala	Tyr	Ile	Asn	Tyr	Asp	Ser	Phe	
			805						810					815		
ctg	ttc	aac	ggg	aac	tac	ctg	agc	ctc	cag	cca	gca	tcc	ggc	ttc	ttc	2496
Leu	Phe	Asn	Gly	Asn	Tyr	Leu	Ser	Leu	Gln	Pro	Ala	Ser	Gly	Phe	Phe	
			820						825				830			
acg	agc	tac	gct	tac	cag	aag	atc	gat	gaa	tcc	acg	ctt	aag	cct	tac	2544
Thr	Ser	Tyr	Ala	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Thr	Leu	Lys	Pro	Tyr	
		835					840						845			
acg	cgc	tac	aag	gtg	tcc	ggg	ttc	atc	ggg	cag	tca	aac	cag	gtt	gaa	2592

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Thr	Arg	Tyr	Lys	Val	Ser	Gly	Phe	Ile	Gly	Gln	Ser	Asn	Gln	Val	Glu	
850						855					860					
ctg	atc	atc	agc	cgc	tac	ggg	aag	gaa	atc	gat	aag	atc	ctt	aac	gtg	2640
Leu	Ile	Ile	Ser	Arg	Tyr	Gly	Lys	Glu	Ile	Asp	Lys	Ile	Leu	Asn	Val	
865					870					875					880	
cca	tac	gca	ggg	cca	ctc	cca	atc	acc	gca	gat	gca	agc	atc	acc	tcg	2688
Pro	Tyr	Ala	Gly	Pro	Leu	Pro	Ile	Thr	Ala	Asp	Ala	Ser	Ile	Thr	Cys	
				885					890					895		
tgc	gct	cca	gaa	ata	ggg	cag	tgc	gat	ggg	gaa	cag	tca	gat	tcc	cat	2736
Cys	Ala	Pro	Glu	Ile	Gly	Gln	Cys	Asp	Gly	Glu	Gln	Ser	Asp	Ser	His	
			900					905					910			
ttc	ttc	aac	tac	agc	atc	gat	gtt	ggc	gca	ctc	cat	cca	gaa	ctt	aac	2784
Phe	Phe	Asn	Tyr	Ser	Ile	Asp	Val	Gly	Ala	Leu	His	Pro	Glu	Leu	Asn	
		915					920					925				
cca	ggg	atc	gaa	atc	ggg	ctg	aag	atc	gtt	cag	agc	aac	ggc	tac	atc	2832
Pro	Gly	Ile	Glu	Ile	Gly	Leu	Lys	Ile	Val	Gln	Ser	Asn	Gly	Tyr	Ile	
		930				935						940				
acc	atc	tcc	aac	ctt	gaa	atc	atc	gaa	gaa	aga	cca	tta	acg	gaa	atg	2880
Thr	Ile	Ser	Asn	Leu	Glu	Ile	Ile	Glu	Glu	Arg	Pro	Leu	Thr	Glu	Met	
					950					955					960	
gaa	att	caa	gca	gtg	aac	cgc	aag	aac	cag	aag	tgg	gaa	cgc	gaa	aag	2928
Glu	Ile	Gln	Ala	Val	Asn	Arg	Lys	Asn	Gln	Lys	Trp	Glu	Arg	Glu	Lys	
				965					970					975		
ctg	ctt	gaa	tgc	gca	tcc	atc	tcc	gaa	ctc	ctc	cag	cct	atc	atc	aac	2976
Leu	Leu	Glu	Cys	Ala	Ser	Ile	Ser	Glu	Leu	Gln	Pro	Ile	Ile	Asn		
			980					985					990			
cag	ata	gat	agc	ctc	ttc	aag	gat	ggc	aac	tgg	tac	aac	gat	atc	cta	3024
Gln	Ile	Asp	Ser	Leu	Phe	Lys	Asp	Gly	Asn	Trp	Tyr	Asn	Asp	Ile	Leu	
		995				1000						1005				
cca	cat	gtt	acc	tac	cag	gat	ctt	aag	aac	atc	atc	atc	cca	gaa	ctt	3072
Pro	His	Val	Thr	Tyr	Gln	Asp	Leu	Lys	Asn	Ile	Ile	Ile	Pro	Glu	Leu	
	1010					1015						1020				
cct	aag	ctc	aag	cat	tgg	ttc	atc	gaa	aac	ctg	cct	ggg	gaa	tac	cat	3120
Pro	Lys	Leu	Lys	His	Trp	Phe	Ile	Glu	Asn	Leu	Pro	Gly	Glu	Tyr	His	
	1025				1030					1035				1040		
gaa	atc	gaa	cag	aag	atg	aag	gaa	gca	tta	aag	tac	gca	ttc	act	cag	3168
Glu	Ile	Glu	Gln	Lys	Met	Lys	Glu	Ala	Leu	Lys	Tyr	Ala	Phe	Thr	Gln	
				1045				1050					1055			
ctc	gat	gaa	aag	aac	ctg	atc	cat	aac	ggc	cat	ttc	acc	acc	aac	ctc	3216
Leu	Asp	Glu	Lys	Asn	Leu	Ile	His	Asn	Gly	His	Phe	Thr	Thr	Asn	Leu	
			1060					1065					1070			
atc	gat	tgg	cag	gtg	gaa	ggc	gat	gct	cag	atg	aag	gtg	ctt	gaa	aac	3264
Ile	Asp	Trp	Gln	Val	Glu	Gly	Asp	Ala	Gln	Met	Lys	Val	Leu	Glu	Asn	
		1075				1080						1085				
gat	gca	ctc	gct	ctc	cag	cta	ttc	aac	tgg	gat	gct	tcc	gca	tcc	cag	3312
Asp	Ala	Leu	Ala	Leu	Gln	Leu	Phe	Asn	Trp	Asp	Ala	Ser	Ala	Ser	Gln	
		1090				1095						1100				
agc	atc	aac	atc	cta	gag	ttc	gat	gaa	gat	aag	gct	tac	aag	ctg	cgt	3360
Ser	Ile	Asn	Ile	Leu	Glu	Phe	Asp	Glu	Asp	Lys	Ala	Tyr	Lys	Leu	Arg	
		1105			1110					1115				1120		
gtg	tac	gca	cag	ggc	tcc	ggg	acg	atc	cag	ttc	ggc	aac	tgc	gaa	gat	3408
Val	Tyr	Ala	Gln	Gly	Ser	Gly	Thr	Ile	Gln	Phe	Gly	Asn	Cys	Glu	Asp	
				1125				1130					1135			
gaa	gct	atc	cag	ttc	aac	acc	aac	tca	ttc	atc	tac	cag	gaa	aag	ata	3456
Glu	Ala	Ile	Gln	Phe	Asn	Thr	Asn	Ser	Phe	Ile	Tyr	Gln	Glu	Lys	Ile	
			1140					1145					1150			
gtg	tac	ttc	gat	acg	cca	tcc	gtt	aac	ctt	cat	atc	cag	agc	gaa	ggc	3504

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Val Tyr Phe Asp Thr Pro Ser Val Asn Leu His Ile Gln Ser Glu Gly	
1155 1160 1165	
tcc gag ttc atc gtg agc agc atc gat ctc atc gaa ctc agc gat gat	3552
Ser Glu Phe Ile Val Ser Ser Ile Asp Leu Ile Glu Leu Ser Asp Asp	
1170 1175 1180	
cag aag gat gaa ctg taa	3570
Gln Lys Asp Glu Leu *	
1185	

<210> SEQ ID NO 33
 <211> LENGTH: 1189
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: SYNAXMI-031(FL)-ER

<400> SEQUENCE: 33

Met Asp Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val Leu	
1 5 10 15	
Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp	
20 25 30	
Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu	
35 40 45	
Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn	
50 55 60	
Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val	
65 70 75 80	
Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp	
85 90 95	
Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn	
100 105 110	
Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp	
115 120 125	
Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser	
130 135 140	
Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr	
145 150 155 160	
Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr	
165 170 175	
Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn	
180 185 190	
Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro	
195 200 205	
Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr	
210 215 220	
Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala	
225 230 235 240	
Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met	
245 250 255	
Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys	
260 265 270	
Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp	
275 280 285	
Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp Ile	

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290	295	300
Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr 305 310 315 320		
Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu 325 330 335		
Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe 340 345 350		
Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser 355 360 365		
Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro 370 375 380		
Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn 385 390 395 400		
Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser 405 410 415		
Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn Ala 420 425 430		
Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile 435 440 445		
Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu 450 455 460		
Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys 465 470 475 480		
Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr 485 490 495		
Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser 500 505 510		
Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp 515 520 525		
Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly 530 535 540		
Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn 545 550 555 560		
Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr 565 570 575		
Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala 580 585 590		
Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly 595 600 605		
Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met 610 615 620		
Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn 625 630 635 640		
Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly 645 650 655		
Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp 660 665 670		
Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn Asn 675 680 685		
Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val Cys 690 695 700		

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Ala	Ile	Ala	Gly	Thr	Gln	Gln	Ser	Cys	Ser	Gly	Pro	Pro	Lys	Phe	Glu
705					710					715					720
Gln	Val	Ser	Asp	Leu	Glu	Lys	Ile	Thr	Thr	Gln	Val	Tyr	Met	Leu	Phe
			725						730					735	
Lys	Ser	Ser	Pro	Tyr	Glu	Glu	Leu	Ala	Leu	Glu	Val	Ser	Ser	Tyr	Gln
			740					745					750		
Ile	Ser	Gln	Val	Ala	Leu	Lys	Val	Met	Ala	Leu	Ser	Asp	Glu	Leu	Phe
	755						760					765			
Cys	Glu	Glu	Lys	Asn	Val	Leu	Arg	Lys	Leu	Val	Asn	Lys	Ala	Lys	Gln
	770					775					780				
Leu	Leu	Glu	Ala	Ser	Asn	Leu	Leu	Val	Gly	Gly	Asn	Phe	Glu	Thr	Thr
785					790					795					800
Gln	Asn	Trp	Val	Leu	Gly	Thr	Asn	Ala	Tyr	Ile	Asn	Tyr	Asp	Ser	Phe
			805						810					815	
Leu	Phe	Asn	Gly	Asn	Tyr	Leu	Ser	Leu	Gln	Pro	Ala	Ser	Gly	Phe	Phe
			820					825					830		
Thr	Ser	Tyr	Ala	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Thr	Leu	Lys	Pro	Tyr
	835						840					845			
Thr	Arg	Tyr	Lys	Val	Ser	Gly	Phe	Ile	Gly	Gln	Ser	Asn	Gln	Val	Glu
	850					855					860				
Leu	Ile	Ile	Ser	Arg	Tyr	Gly	Lys	Glu	Ile	Asp	Lys	Ile	Leu	Asn	Val
865					870					875					880
Pro	Tyr	Ala	Gly	Pro	Leu	Pro	Ile	Thr	Ala	Asp	Ala	Ser	Ile	Thr	Cys
			885						890					895	
Cys	Ala	Pro	Glu	Ile	Gly	Gln	Cys	Asp	Gly	Glu	Gln	Ser	Asp	Ser	His
			900					905					910		
Phe	Phe	Asn	Tyr	Ser	Ile	Asp	Val	Gly	Ala	Leu	His	Pro	Glu	Leu	Asn
	915					920						925			
Pro	Gly	Ile	Glu	Ile	Gly	Leu	Lys	Ile	Val	Gln	Ser	Asn	Gly	Tyr	Ile
	930					935					940				
Thr	Ile	Ser	Asn	Leu	Glu	Ile	Ile	Glu	Glu	Arg	Pro	Leu	Thr	Glu	Met
945					950					955					960
Glu	Ile	Gln	Ala	Val	Asn	Arg	Lys	Asn	Gln	Lys	Trp	Glu	Arg	Glu	Lys
			965						970					975	
Leu	Leu	Glu	Cys	Ala	Ser	Ile	Ser	Glu	Leu	Leu	Gln	Pro	Ile	Ile	Asn
			980					985					990		
Gln	Ile	Asp	Ser	Leu	Phe	Lys	Asp	Gly	Asn	Trp	Tyr	Asn	Asp	Ile	Leu
	995					1000						1005			
Pro	His	Val	Thr	Tyr	Gln	Asp	Leu	Lys	Asn	Ile	Ile	Ile	Pro	Glu	Leu
	1010					1015					1020				
Pro	Lys	Leu	Lys	His	Trp	Phe	Ile	Glu	Asn	Leu	Pro	Gly	Glu	Tyr	His
1025					1030					1035					1040
Glu	Ile	Glu	Gln	Lys	Met	Lys	Glu	Ala	Leu	Lys	Tyr	Ala	Phe	Thr	Gln
			1045					1050						1055	
Leu	Asp	Glu	Lys	Asn	Leu	Ile	His	Asn	Gly	His	Phe	Thr	Thr	Asn	Leu
	1060							1065					1070		
Ile	Asp	Trp	Gln	Val	Glu	Gly	Asp	Ala	Gln	Met	Lys	Val	Leu	Glu	Asn
	1075					1080						1085			
Asp	Ala	Leu	Ala	Leu	Gln	Leu	Phe	Asn	Trp	Asp	Ala	Ser	Ala	Ser	Gln
	1090					1095					1100				

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Ser Ile Asn Ile Leu Glu Phe Asp Glu Asp Lys Ala Tyr Lys Leu Arg
 1105 1110 1115 1120

Val Tyr Ala Gln Gly Ser Gly Thr Ile Gln Phe Gly Asn Cys Glu Asp
 1125 1130 1135

Glu Ala Ile Gln Phe Asn Thr Asn Ser Phe Ile Tyr Gln Glu Lys Ile
 1140 1145 1150

Val Tyr Phe Asp Thr Pro Ser Val Asn Leu His Ile Gln Ser Glu Gly
 1155 1160 1165

Ser Glu Phe Ile Val Ser Ser Ile Asp Leu Ile Glu Leu Ser Asp Asp
 1170 1175 1180

Gln Lys Asp Glu Leu
 1185

<210> SEQ ID NO 34
 <211> LENGTH: 3669
 <212> TYPE: DNA
 <213> ORGANISM: Unknown
 <220> FEATURE:
 <223> OTHER INFORMATION: isolated from soil sample (AXMI-049)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(3669)

<400> SEQUENCE: 34

atg gat gac atg aca aat tta tcc gat gta tat tca ccc gta cct tcc Met Asp Asp Met Thr Asn Leu Ser Asp Val Tyr Ser Pro Val Pro Ser 1 5 10 15	48
aat gta tta gca gct cca ctt att ctt gaa gaa aca aag aaa aaa aca Asn Val Leu Ala Ala Pro Leu Ile Leu Glu Glu Thr Lys Lys Lys Thr 20 25 30	96
ccg gct gaa caa gca aaa gaa gat tta gaa aag gca ttg aga aca gga Pro Ala Glu Gln Ala Lys Glu Asp Leu Glu Lys Ala Leu Arg Thr Gly 35 40 45	144
aag ttt tcc gat gca att gca caa att tta aat gat gtt ctt att aac Lys Phe Ser Ser Asp Ala Ile Ala Gln Ile Leu Asn Asp Val Leu Ile Asn 50 55 60	192
caa aag ttc agc tat caa aca gcg gtt aca gtt tcc tta tct ttg gct Gln Lys Phe Ser Tyr Gln Thr Ala Val Thr Val Ser Leu Ser Leu Ala 65 70 75 80	240
agt ata gtt ctt cca gaa ata ggt ttt ttt gcc ccc ttt gtt ggt tta Ser Ile Val Leu Pro Glu Ile Gly Phe Phe Ala Pro Phe Val Gly Leu 85 90 95	288
ttt ttt tct gct tta aat aaa tct caa aat ata cct acg act tca gat Phe Phe Ser Ala Leu Asn Lys Ser Gln Asn Ile Pro Thr Thr Ser Asp 100 105 110	336
att ttt gaa gcg atg aaa cca gct att caa aca atg att gat cgt agt Ile Phe Glu Ala Met Lys Pro Ala Ile Gln Thr Met Ile Asp Arg Ser 115 120 125	384
tta aca gat gct gaa aac aag gag atg gat gat cag gcg cac aac cta Leu Thr Asp Ala Glu Asn Lys Glu Met Asp Asp Gln Ala His Asn Leu 130 135 140	432
ttt acg cga tta caa act tat caa gag caa ata gat ctc tat aaa cat Phe Thr Arg Leu Gln Thr Tyr Gln Glu Gln Ile Asp Leu Tyr Lys His 145 150 155 160	480
att tta gat gca aaa caa aaa cca act ctt aac gat ata gga gat ctt Ile Leu Asp Ala Lys Gln Lys Pro Thr Leu Asn Asp Ile Gly Asp Leu 165 170 175	528
cac act tcg atc gac gaa act ctc aga aca tta gat tcc aat tta gca	576

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His	Thr	Ser	Ile	Asp	Glu	Thr	Leu	Arg	Thr	Leu	Asp	Ser	Asn	Leu	Ala	
			180					185					190			
ttt	ttc	caa	aca	gaa	ggc	tat	caa	gat	ctc	ggg	tta	cca	tat	tac	aca	624
Phe	Phe	Gln	Thr	Glu	Gly	Tyr	Gln	Asp	Leu	Gly	Leu	Pro	Tyr	Tyr	Thr	
		195					200					205				
att	ttt	gcc	aca	caa	tat	ttg	tta	atc	ctt	tca	gat	aaa	att	aaa	act	672
Ile	Phe	Ala	Thr	Gln	Tyr	Leu	Leu	Ile	Leu	Ser	Asp	Lys	Ile	Lys	Thr	
		210				215					220					
ggg	atc	aca	tggt	gga	tat	aat	cct	att	aac	att	cca	gat	ttt	caa	aac	720
Gly	Ile	Thr	Trp	Gly	Tyr	Asn	Pro	Ile	Asn	Ile	Pro	Asp	Phe	Gln	Asn	
225					230					235				240		
caa	ttt	aat	aat	aga	ata	ctt	tta	ttt	aca	aaa	tac	att	agt	ggg	caa	768
Gln	Phe	Asn	Asn	Arg	Ile	Leu	Leu	Phe	Thr	Lys	Tyr	Ile	Ser	Gly	Gln	
				245					250					255		
ctt	aag	aaa	atg	tat	gac	aac	ggg	gta	cat	cca	gca	ctt	tta	tat	caa	816
Leu	Lys	Lys	Met	Tyr	Asp	Asn	Gly	Val	His	Pro	Ala	Leu	Leu	Tyr	Gln	
			260					265					270			
aac	tgt	atc	caa	ttt	gtt	gct	tta	tggt	cct	act	ttt	tct	ccc	gca	gat	864
Asn	Cys	Ile	Gln	Phe	Val	Ala	Leu	Trp	Pro	Thr	Phe	Ser	Pro	Ala	Asp	
		275					280					285				
tat	aac	ctt	agt	aac	agc	aca	gat	tta	gaa	caa	aca	ata	agt	ttt	aag	912
Tyr	Asn	Leu	Ser	Asn	Ser	Thr	Asp	Leu	Glu	Gln	Thr	Ile	Ser	Phe	Lys	
		290				295					300					
agt	ttc	atc	tcc	tat	aag	agt	tta	aat	gat	tat	aat	tat	gca	ctt	cct	960
Ser	Phe	Ile	Ser	Tyr	Lys	Ser	Leu	Asn	Asp	Tyr	Asn	Tyr	Ala	Leu	Pro	
305					310					315				320		
gaa	att	aat	aca	tggt	aca	aat	ttt	gaa	atg	aca	aaa	tca	ctt	gat	ttt	1008
Glu	Ile	Asn	Thr	Trp	Thr	Asn	Phe	Glu	Met	Thr	Lys	Ser	Leu	Asp	Phe	
			325						330					335		
aac	aac	tgt	aga	tcc	atg	gat	aat	tat	ggg	atc	gcg	ggg	gac	ctt	cgt	1056
Asn	Asn	Cys	Arg	Ser	Met	Asp	Asn	Tyr	Gly	Ile	Ala	Gly	Asp	Leu	Arg	
			340					345					350			
ata	aca	aat	cat	aaa	aat	gaa	atc	cat	gaa	ata	tct	gct	cct	tcg	gta	1104
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Leu	Tyr	Met	Thr	Ser	Asn	Gln	Cys	Asn	Ser	Arg	Leu	Val	Phe	Pro	Phe	
		370				375					380					
gat	gat	cct	att	gtt	aaa	ttc	gaa	gga	aca	agt	agt	gtt	ttc	ata	ggg	1200
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385					390					395				400		
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aaa	agt	tta	ata	ttc	cct	cct	cct	tca	gga	gtt	aat	caa	caa	ggg	ttc	1296
Lys	Ser	Leu	Ile	Phe	Pro	Pro	Pro	Ser	Gly	Val	Asn	Gln	Gln	Gly	Phe	
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Thr	Gln	Asn	Tyr	Ser	Val	Ile	Pro	His	Pro	Gly	Phe	Lys	Ile	Ala	Gly	
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Ile	Thr	Asn	Met	Ser	Tyr	Leu	Pro	Thr	His	His	Asp	Ser	Asn	Ala	Arg	
		450				455					460					
aca	caa	ata	gaa	cat	atc	caa	gtt	cct	gaa	aaa	atc	ttt	cca	gaa	aat	1440
Thr	Gln	Ile	Glu	His	Ile	Gln	Val	Pro	Glu	Lys	Ile	Phe	Pro	Glu	Asn	
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Gly	Ile	Pro	Ala	Glu	Lys	Gly	Tyr	Gly	Asp	Ser	Ile	Ala	Tyr	Val	Ser	
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gaa	ccg	gta	aat	ggt	gcg	agt	gca	gtt	aaa	ctt	act	tca	aat	caa	att	1584
Glu	Pro	Val	Asn	Gly	Ala	Ser	Ala	Val	Lys	Leu	Thr	Ser	Asn	Gln	Ile	
		515					520					525				
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Leu	Gln	Met	Glu	Ile	Thr	Asn	Val	Thr	Thr	Gln	Lys	Tyr	Gln	Val	Arg	
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ata	cgt	tat	gct	aca	gct	gga	gat	aca	gag	gct	aat	ata	agg	ttc	cat	1680
Ile	Arg	Tyr	Ala	Thr	Ala	Gly	Asp	Thr	Glu	Ala	Asn	Ile	Arg	Phe	His	
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Ile	Ile	Asp	Pro	Asn	Glu	Asn	Asn	Leu	Ile	Asn	Gly	Pro	Asn	His	Phe	
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Thr	Ala	Val	Ser	Asn	Thr	Gln	Thr	Ser	Val	Gln	Gly	Glu	Asn	Gly	Lys	
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tat	gta	cta	aac	aca	ctt	gta	aat	tca	ata	ata	tta	cca	tca	gga	aaa	1824
Tyr	Val	Leu	Asn	Thr	Leu	Val	Asn	Ser	Ile	Ile	Leu	Pro	Ser	Gly	Lys	
		595					600					605				
caa	aag	gtc	ttt	att	caa	aac	act	ggt	tct	caa	gat	ctc	ttt	tta	gac	1872
Gln	Lys	Val	Phe	Ile	Gln	Asn	Thr	Gly	Ser	Gln	Asp	Leu	Phe	Leu	Asp	
	610					615					620					
cgt	att	gaa	ttt	att	cca	tta	caa	cta	gaa	ctt	cct	ttc	act	tca	aaa	1920
Arg	Ile	Glu	Phe	Ile	Pro	Leu	Gln	Leu	Glu	Leu	Pro	Phe	Thr	Ser	Lys	
625					630				635					640		
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Leu	Pro	Glu	Thr	Thr	Thr	Gln	Pro	Asn	Thr	Thr	Lys	Thr	Ile	Trp	Ser	
			645					650						655		
ggt	caa	aaa	cct	gct	aat	aca	ctt	tct	ctt	caa	ggt	aca	gtt	tat	aat	2016
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		660					665						670			
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Asp	Ala	Ser	Ile	Glu	Leu	Gln	Leu	Tyr	Met	Asn	Asp	Asn	Leu	Val	Gln	
		675				680						685				
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Lys	Ile	Pro	Ala	Gln	Gly	Pro	Gly	Pro	Ser	Phe	Asp	Cys	Asp	Asp	Gln	
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tct	aaa	cct	att	aat	caa	cca	aat	ata	aaa	act	gaa	gaa	ttt	aac	aaa	2160
Ser	Lys	Pro	Ile	Asn	Gln	Pro	Asn	Ile	Lys	Thr	Glu	Glu	Phe	Asn	Lys	
	705				710					715				720		
ctt	gtc	tta	aaa	gaa	tta	agt	agt	acc	tat	tcg	tat	tgt	atg	gga	gga	2208
Leu	Val	Leu	Lys	Glu	Leu	Ser	Ser	Thr	Tyr	Ser	Tyr	Cys	Met	Gly	Gly	
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Ala	Phe	Glu	Asn	Thr	Tyr	Gln	Ile	Asp	Ile	Thr	Ile	Asp	Ser	Lys	Ser	
		740						745					750			
caa	tct	ttt	act	act	cca	gaa	gat	tta	gaa	aaa	atc	aca	aac	caa	gtc	2304
Gln	Ser	Phe	Thr	Thr	Pro	Glu	Asp	Leu	Glu	Lys	Ile	Thr	Asn	Gln	Val	
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Asn	Gln	Leu	Phe	Thr	Ser	Ser	Ser	Gln	Thr	Lys	Leu	Val	Gln	Thr	Val	
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Asp	Asp	Val	Phe	Gly	Val	Glu	Lys	Lys	Ala	Leu	Arg	Lys	Leu	Val	Asn	
			805						810					815		
cag	gcc	aaa	caa	tta	agt	aaa	gta	cga	aat	gta	ctg	gtc	ggg	gga	aac	2496
Gln	Ala	Lys	Gln	Leu	Ser	Lys	Val	Arg	Asn	Val	Leu	Val	Gly	Gly	Asn	
			820					825					830			
ttt	gaa	aaa	ggg	cat	aaa	tgg	gta	cta	ggg	cgt	aaa	gcg	aca	acg	gta	2544
Phe	Glu	Lys	Gly	His	Lys	Trp	Val	Leu	Gly	Arg	Lys	Ala	Thr	Thr	Val	
			835				840					845				
gcg	gat	cat	gat	tta	ttc	aaa	ggg	gat	cat	tta	tta	tta	cca	cca	cca	2592
Ala	Asp	His	Asp	Leu	Phe	Lys	Gly	Asp	His	Leu	Leu	Leu	Pro	Pro	Pro	
	850					855				860						
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Thr	Leu	Tyr	Pro	Ser	Tyr	Ala	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	
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aaa	tcc	aat	aca	cgc	tat	acg	gtt	tcc	ggg	ttt	gtt	gcg	caa	agt	gaa	2688
Lys	Ser	Asn	Thr	Arg	Tyr	Thr	Val	Ser	Gly	Phe	Val	Ala	Gln	Ser	Glu	
				885					890					895		
cat	tta	gaa	gtt	gtt	gtt	tct	cgc	tat	ggg	aaa	gaa	gta	aat	acc	ctg	2736
His	Leu	Glu	Val	Val	Val	Ser	Arg	Tyr	Gly	Lys	Glu	Val	Asn	Thr	Leu	
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tta	cat	gtc	cct	tat	gaa	gaa	gca	tta	ccg	att	tct	tcc	gat	gag	cgt	2784
Leu	His	Val	Pro	Tyr	Glu	Glu	Ala	Leu	Pro	Ile	Ser	Ser	Asp	Glu	Arg	
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cca	aat	tgc	tgt	aaa	cca	gct	gct	tgt	cag	tgt	cca	tct	tgc	aat	ggg	2832
Pro	Asn	Cys	Cys	Lys	Pro	Ala	Ala	Cys	Gln	Cys	Pro	Ser	Cys	Asn	Gly	
	930					935					940					
gat	gca	cca	gac	tcc	cat	ttc	ttt	agc	tat	agt	atc	gat	gtt	ggg	tcc	2880
Asp	Ala	Pro	Asp	Ser	His	Phe	Phe	Ser	Tyr	Ser	Ile	Asp	Val	Gly	Ser	
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tta	caa	gca	gat	gta	aat	tta	gga	att	gag	ttt	ggg	ctt	cgt	att	gtg	2928
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aaa	tcc	aac	gga	ttt	gca	aaa	atc	agt	aac	cta	gaa	atc	aaa	gaa	gac	2976
Lys	Ser	Asn	Gly	Phe	Ala	Lys	Ile	Ser	Asn	Leu	Glu	Ile	Lys	Glu	Asp	
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Arg	Pro	Leu	Thr	Glu	Lys	Glu	Ile	Lys	Lys	Ile	Gln	Arg	Lys	Glu	Gln	
		995				1000						1005				
aag	tgg	aaa	aaa	gca	ttt	gac	aaa	gaa	cag	gca	gag	tta	acg	gca	aca	3072
Lys	Trp	Lys	Lys	Ala	Phe	Asp	Lys	Glu	Gln	Ala	Glu	Leu	Thr	Ala	Thr	
	1010					1015					1020					
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Leu	Gln	Pro	Thr	Leu	Asn	Gln	Ile	Asn	Ala	Leu	Tyr	Gln	Asn	Glu	Asp	
	1025				1030				1035						1040	
tgg	aac	ggg	tcg	att	cac	cct	cat	gta	acg	tat	caa	cat	cta	tcc	gat	3168
Trp	Asn	Gly	Ser	Ile	His	Pro	His	Val	Thr	Tyr	Gln	His	Leu	Ser	Asp	
				1045				1050					1055			
gtt	gtc	gta	cca	gca	tta	cca	aaa	caa	aga	cat	tgg	ttt	atg	gaa	gat	3216
Val	Val	Val	Pro	Ala	Leu	Pro	Lys	Gln	Arg	His	Trp	Phe	Met	Glu	Asp	
			1060					1065					1070			
cga	caa	ggg	gaa	cat	tac	aat	gta	aca	caa	caa	ttc	caa	caa	gca	tta	3264
Arg	Gln	Gly	Glu	His	Tyr	Asn	Val	Thr	Gln	Gln	Phe	Gln	Gln	Ala	Leu	
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<211> LENGTH: 1223
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: isolated from soil sample (AXMI-049)
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Pro	Ala	Glu	Gln	Ala	Lys	Glu	Asp	Leu	Glu	Lys	Ala	Leu	Arg	Thr	Gly
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Gln	Lys	Phe	Ser	Tyr	Gln	Thr	Ala	Val	Thr	Val	Ser	Leu	Ser	Leu	Ala
65					70					75					80
Ser	Ile	Val	Leu	Pro	Glu	Ile	Gly	Phe	Phe	Ala	Pro	Phe	Val	Gly	Leu
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Phe	Phe	Ser	Ala	Leu	Asn	Lys	Ser	Gln	Asn	Ile	Pro	Thr	Thr	Ser	Asp
			100					105					110		
Ile	Phe	Glu	Ala	Met	Lys	Pro	Ala	Ile	Gln	Thr	Met	Ile	Asp	Arg	Ser
			115				120					125			
Leu	Thr	Asp	Ala	Glu	Asn	Lys	Glu	Met	Asp	Asp	Gln	Ala	His	Asn	Leu
	130					135					140				
Phe	Thr	Arg	Leu	Gln	Thr	Tyr	Gln	Glu	Gln	Ile	Asp	Leu	Tyr	Lys	His
145					150					155					160
Ile	Leu	Asp	Ala	Lys	Gln	Lys	Pro	Thr	Leu	Asn	Asp	Ile	Gly	Asp	Leu

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165							170					175			
His	Thr	Ser	Ile	Asp	Glu	Thr	Leu	Arg	Thr	Leu	Asp	Ser	Asn	Leu	Ala
			180					185					190		
Phe	Phe	Gln	Thr	Glu	Gly	Tyr	Gln	Asp	Leu	Gly	Leu	Pro	Tyr	Tyr	Thr
		195					200					205			
Ile	Phe	Ala	Thr	Gln	Tyr	Leu	Leu	Ile	Leu	Ser	Asp	Lys	Ile	Lys	Thr
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Gly	Ile	Thr	Trp	Gly	Tyr	Asn	Pro	Ile	Asn	Ile	Pro	Asp	Phe	Gln	Asn
225					230					235					240
Gln	Phe	Asn	Asn	Arg	Ile	Leu	Leu	Phe	Thr	Lys	Tyr	Ile	Ser	Gly	Gln
				245					250					255	
Leu	Lys	Lys	Met	Tyr	Asp	Asn	Gly	Val	His	Pro	Ala	Leu	Leu	Tyr	Gln
			260					265					270		
Asn	Cys	Ile	Gln	Phe	Val	Ala	Leu	Trp	Pro	Thr	Phe	Ser	Pro	Ala	Asp
		275					280					285			
Tyr	Asn	Leu	Ser	Asn	Ser	Thr	Asp	Leu	Glu	Gln	Thr	Ile	Ser	Phe	Lys
	290					295					300				
Ser	Phe	Ile	Ser	Tyr	Lys	Ser	Leu	Asn	Asp	Tyr	Asn	Tyr	Ala	Leu	Pro
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Glu	Ile	Asn	Thr	Trp	Thr	Asn	Phe	Glu	Met	Thr	Lys	Ser	Leu	Asp	Phe
				325					330					335	
Asn	Asn	Cys	Arg	Ser	Met	Asp	Asn	Tyr	Gly	Ile	Ala	Gly	Asp	Leu	Arg
			340					345					350		
Ile	Thr	Asn	His	Lys	Asn	Glu	Ile	His	Glu	Ile	Ser	Ala	Pro	Ser	Val
		355					360					365			
Leu	Tyr	Met	Thr	Ser	Asn	Gln	Cys	Asn	Ser	Arg	Leu	Val	Phe	Pro	Phe
	370					375					380				
Asp	Asp	Pro	Ile	Val	Lys	Phe	Glu	Gly	Thr	Ser	Ser	Val	Phe	Ile	Gly
385					390					395					400
Thr	Pro	Gly	Leu	Pro	Gln	Phe	Tyr	Thr	Asn	Phe	Gln	Leu	Thr	Ser	Gly
				405					410					415	
Lys	Ser	Leu	Ile	Phe	Pro	Pro	Pro	Ser	Gly	Val	Asn	Gln	Gln	Gly	Phe
			420					425				430			
Thr	Gln	Asn	Tyr	Ser	Val	Ile	Pro	His	Pro	Gly	Phe	Lys	Ile	Ala	Gly
		435					440					445			
Ile	Thr	Asn	Met	Ser	Tyr	Leu	Pro	Thr	His	His	Asp	Ser	Asn	Ala	Arg
	450					455					460				
Thr	Gln	Ile	Glu	His	Ile	Gln	Val	Pro	Glu	Lys	Ile	Phe	Pro	Glu	Asn
465					470					475					480
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				485				490						495	
Gly	Ile	Pro	Ala	Glu	Lys	Gly	Tyr	Gly	Asp	Ser	Ile	Ala	Tyr	Val	Ser
			500					505					510		
Glu	Pro	Val	Asn	Gly	Ala	Ser	Ala	Val	Lys	Leu	Thr	Ser	Asn	Gln	Ile
		515					520					525			
Leu	Gln	Met	Glu	Ile	Thr	Asn	Val	Thr	Thr	Gln	Lys	Tyr	Gln	Val	Arg
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Ile	Arg	Tyr	Ala	Thr	Ala	Gly	Asp	Thr	Glu	Ala	Asn	Ile	Arg	Phe	His
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Ile	Ile	Asp	Pro	Asn	Glu	Asn	Asn	Leu	Ile	Asn	Gly	Pro	Asn	His	Phe
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Gln	Lys	Val	Phe	Ile	Gln	Asn	Thr	Gly	Ser	Gln	Asp	Leu	Phe	Leu	Asp	610	615	620
Arg	Ile	Glu	Phe	Ile	Pro	Leu	Gln	Leu	Glu	Leu	Pro	Phe	Thr	Ser	Lys	625	630	635
Leu	Pro	Glu	Thr	Thr	Thr	Gln	Pro	Asn	Thr	Thr	Lys	Thr	Ile	Trp	Ser	645	650	655
Gly	Gln	Lys	Pro	Ala	Asn	Thr	Leu	Ser	Leu	Gln	Gly	Thr	Val	Tyr	Asn	660	665	670
Asp	Ala	Ser	Ile	Glu	Leu	Gln	Leu	Tyr	Met	Asn	Asp	Asn	Leu	Val	Gln	675	680	685
Lys	Ile	Pro	Ala	Gln	Gly	Pro	Gly	Pro	Ser	Phe	Asp	Cys	Asp	Asp	Gln	690	695	700
Ser	Lys	Pro	Ile	Asn	Gln	Pro	Asn	Ile	Lys	Thr	Glu	Glu	Phe	Asn	Lys	705	710	715
Leu	Val	Leu	Lys	Glu	Leu	Ser	Ser	Thr	Tyr	Ser	Tyr	Cys	Met	Gly	Gly	725	730	735
Ala	Phe	Glu	Asn	Thr	Tyr	Gln	Ile	Asp	Ile	Thr	Ile	Asp	Ser	Lys	Ser	740	745	750
Gln	Ser	Phe	Thr	Thr	Pro	Glu	Asp	Leu	Glu	Lys	Ile	Thr	Asn	Gln	Val	755	760	765
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Thr	Asp	Tyr	Gly	Ile	Asp	Gln	Met	Val	Met	Lys	Val	Asp	Ala	Leu	Ser	785	790	795
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Gln	Ala	Lys	Gln	Leu	Ser	Lys	Val	Arg	Asn	Val	Leu	Val	Gly	Gly	Asn	820	825	830
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Ala	Asp	His	Asp	Leu	Phe	Lys	Gly	Asp	His	Leu	Leu	Leu	Pro	Pro	Pro	850	855	860
Thr	Leu	Tyr	Pro	Ser	Tyr	Ala	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Lys	Leu	865	870	875
Lys	Ser	Asn	Thr	Arg	Tyr	Thr	Val	Ser	Gly	Phe	Val	Ala	Gln	Ser	Glu	885	890	895
His	Leu	Glu	Val	Val	Val	Ser	Arg	Tyr	Gly	Lys	Glu	Val	Asn	Thr	Leu	900	905	910
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Asp	Ala	Pro	Asp	Ser	His	Phe	Phe	Ser	Tyr	Ser	Ile	Asp	Val	Gly	Ser	945	950	955
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 Arg Pro Leu Thr Glu Lys Glu Ile Lys Lys Ile Gln Arg Lys Glu Gln
 995 1000 1005
 Lys Trp Lys Lys Ala Phe Asp Lys Glu Gln Ala Glu Leu Thr Ala Thr
 1010 1015 1020
 Leu Gln Pro Thr Leu Asn Gln Ile Asn Ala Leu Tyr Gln Asn Glu Asp
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 Trp Asn Gly Ser Ile His Pro His Val Thr Tyr Gln His Leu Ser Asp
 1045 1050 1055
 Val Val Val Pro Ala Leu Pro Lys Gln Arg His Trp Phe Met Glu Asp
 1060 1065 1070
 Arg Gln Gly Glu His Tyr Asn Val Thr Gln Gln Phe Gln Gln Ala Leu
 1075 1080 1085
 Asp Arg Ala Phe Gln Gln Ile Glu Glu Gln Asn Leu Ile His Asn Gly
 1090 1095 1100
 Ser Phe Ala Asn Gly Leu Thr Asp Trp Thr Val Thr Gly Asp Ala His
 1105 1110 1115 1120
 Val Thr Ile Gln Asp Asp Asp Gln Val Leu Glu Leu Ser His Trp Asp
 1125 1130 1135
 Ala Ser Val Ser Gln Thr Ile Glu Ile Ile Asp Phe Glu Glu Glu Lys
 1140 1145 1150
 Glu Tyr Lys Leu Arg Val Arg Gly Lys Gly Lys Gly Thr Val Thr Val
 1155 1160 1165
 Gln His Gly Glu Glu Glu Leu Glu Thr Met Thr Phe Asn Ala Thr Ser
 1170 1175 1180
 Phe Thr Thr Gln Glu Gln Thr Phe Tyr Phe Glu Gly Asn Thr Val Asp
 1185 1190 1195 1200
 Ile His Val Gln Ser Glu Asn Asn Thr Phe Leu Val Asp Ser Val Glu
 1205 1210 1215
 Leu Ile Glu Ile Ile Glu Lys
 1220

<210> SEQ ID NO 36
 <211> LENGTH: 4
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Targeting peptide

<400> SEQUENCE: 36

Lys Asp Glu Leu
 1

<210> SEQ ID NO 37
 <211> LENGTH: 3657
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: aposynaxmi-031(fl)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)...(3657)

<400> SEQUENCE: 37

atg cag atc ctt ggg tac tcc agc ttc gtt gct atc gct ctt ctt atg
 Met Gln Ile Leu Gly Tyr Ser Ser Phe Val Ala Ile Ala Leu Leu Met

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1	5	10	15	
agc gtg gtt gtt gtt tgc aat ggg ggc aag acg tcc acc tac gtg cgt				96
Ser Val Val Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg				
	20	25	30	
aat ctg gat tgc aat ctc cag agc cag cag aat atc cca tac aat gtg				144
Asn Leu Asp Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val				
	35	40	45	
ctt gct atc cct gtt agc aat gtt aat agc ctt acg gat acg gtt ggc				192
Leu Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly				
	50	55	60	
gat cta aag aag gca tgg gaa gag ttc cag aag acg ggc agc ttc tcc				240
Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser				
	65	70	75	80
ctt acc gca ctc cag cag ggc ttc agc gct tcc cag ggc ggg acg ttc				288
Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe				
	85	90	95	
aat tac ctc acc ctc ctc cag tcc ggg atc tcc ctg gct ggc agc ttc				336
Asn Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe				
	100	105	110	
gtg cct ggc ggc acc ttc gtt gct cca atc atc aat atg gtg atc ggc				384
Val Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly				
	115	120	125	
tgg ctc tgg cct cat aag aat aag aat gca gat acg gaa aat ctg atc				432
Trp Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile				
	130	135	140	
aat ctg atc gat tca gaa atc cag aag cag ctg aat aag gct ctg ctg				480
Asn Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu				
	145	150	155	160
gat gct gat cgc aat gaa tgg agc agc tac ctc gag tcc atc ttc gat				528
Asp Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp				
	165	170	175	
agc agc aat aat ctg aat ggc gca atc gtt gat gct cag tgg tcc ggc				576
Ser Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly				
	180	185	190	
acc gtg aat acg acc aat cgt acg ctt cgt aat cct acg gaa tca gat				624
Thr Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp				
	195	200	205	
tac acc aat gtg gtg acg aat ttc atc gca gca gat ggg gat atc gct				672
Tyr Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala				
	210	215	220	
aat aat gaa aat cat atc atg aat ggg aat ttc gat gtg gca gca gct				720
Asn Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala				
	225	230	235	240
cca tac ttc gtt atc ggg gct acc gct aga ttc gca gct atg cag tcc				768
Pro Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser				
	245	250	255	
tac atc aag ttc tgc aat gca tgg atc gat aag gtt ggg ctg tca gat				816
Tyr Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp				
	260	265	270	
gct cag ctg acc acg cag aag gct aat ctg gat aga acg aag cag aat				864
Ala Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn				
	275	280	285	
atg cgt aat gct atc ctt aat tac acc cag cag gtt atg aag gtt ttc				912
Met Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe				
	290	295	300	
aag gat tcc aag aat atg cca acg atc ggc acg aat aag ttc agc gtt				960
Lys Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val				

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305	310	315	320	
gat acc tac aat gtt tac atc aag ggg atg acg ctt aat gtg ctt gat Asp Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp	325	330	335	1008
atc gtt gct atc tgg cca agc ctg tac cca gat gat tac acg tca cag Ile Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln	340	345	350	1056
acg gct ctg gaa cag acc cgc gtg acg ttc tcc aat atg gtg ggg cag Thr Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln	355	360	365	1104
gaa gaa ggc acg gat ggc agc ctc aga atc tac aat acc ttc gat agc Glu Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser	370	375	380	1152
ttc tcc tac cag cat agc cct atc cct aat aat aat gtg aat ctc atc Phe Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile	385	390	395	1200
agc tac tac aat gat gaa ctt cag aat ctg gaa ctc ggg gtt tac acc Ser Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr	405	410	415	1248
cca cca aag aag ggc tca ggc tac agc tac cca tac ggg ttc gtg ctg Pro Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu	420	425	430	1296
aat tac gca aat agc aag tac aag tac ggc gat tcc aat gat cca gaa Asn Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu	435	440	445	1344
tcc ctc ggc ggg ctt tcc acc ctt agc gct cca atc caa cag gtt aat Ser Leu Gly Gly Leu Ser Thr Leu Ser Ala Pro Ile Gln Gln Val Asn	450	455	460	1392
gct gct acc cag aat agc aag tac ctt gat ggc gaa atc ctg aat ggg Ala Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly	465	470	475	1440
atc ggc gca agc ctg cct ggc tac tgc acg acc ggg tgc tca cct acc Ile Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr	485	490	495	1488
gaa cca cca ttc agc tgc acg agc acg gca aat ggg tac aag gca agc Glu Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser	500	505	510	1536
tgc aat cca agc gat acc aat cag aag atc aat gct ctc tac cca ttc Cys Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe	515	520	525	1584
acg cag gca aat gtg aag ggg aat acc ggg aag ctg ggc gtt ctc gca Thr Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala	530	535	540	1632
agc ctt gtt agc tac gat ctg aat cct aag aat gtt ttc ggg gaa ctc Ser Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu	545	550	555	1680
gat tca gat acc aat aat gtt atc ctt aag ggc atc cca gca gaa aag Asp Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys	565	570	575	1728
ggc tac ttc cca aat aat gca aga cca acc gtt gtg aag gaa tgg atc Gly Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile	580	585	590	1776
aat ggg gct tcc gca gtt cca ctt gat tcc ggc aat acc ctg ttc atg Asn Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met	595	600	605	1824
acg gct acg aac ctg acg gct acc cag tac aga atc cgc atc cgt tac Thr Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr				1872

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610	615	620	
gct aac cca aac tca aac acg cag atc ggc gtt aga atc acg cag aac			1920
Ala Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn			
625	630	635	640
ggg agc ctc atc tcc tcc tcc aac ctc acg ctg tac tca acc acc gat			1968
Gly Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp			
	645	650	655
atg aac aac acc ctg cca ctg aac gtt tac gtg atc ggg gaa aac ggg			2016
Met Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly			
	660	665	670
aac tac acc ctc cag gat ctc tac aac acg acg aac gtt ctg tcc acg			2064
Asn Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr			
	675	680	685
ggc gat atc acc ctg cag atc acc ggc ggg gat cag aag ata ttc atc			2112
Gly Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile			
	690	695	700
gat cgc atc gag ttc gtg cct acg atg cca gtg cca ggc aac acc aac			2160
Asp Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn			
	705	710	715
aac aac aac ggg aac aac aac ggc aac aac aac cct cct cat cat gtt			2208
Asn Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val			
	725	730	735
tgc gct atc gca ggc acc cag cag tcc tgc tcc ggc cca cca aag ttc			2256
Cys Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe			
	740	745	750
gag cag gtg tcc gat tta gaa aag ata acc acg cag gtt tac atg ctc			2304
Glu Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu			
	755	760	765
ttc aag tcc tcc cca tac gaa gaa ctt gct ctt gaa gtt agc agc tac			2352
Phe Lys Ser Ser Pro Tyr Glu Glu Leu Ala Leu Glu Val Ser Ser Tyr			
	770	775	780
cag atc agc cag gtt gca ctg aag gtt atg gct ctc agc gat gaa cta			2400
Gln Ile Ser Gln Val Ala Leu Lys Val Met Ala Leu Ser Asp Glu Leu			
	785	790	800
ttc tgc gaa gaa aag aac gtg ctg aga aag ctc gtg aac aag gca aag			2448
Phe Cys Glu Glu Lys Asn Val Leu Arg Lys Leu Val Asn Lys Ala Lys			
	805	810	815
cag ctt ctc gaa gca agc aac ctt ctc gtt ggg ggg aac ttc gag acg			2496
Gln Leu Leu Glu Ala Ser Asn Leu Leu Val Gly Gly Asn Phe Glu Thr			
	820	825	830
act cag aac tgg gtg ctc ggc acg aac gct tac atc aac tat gat tca			2544
Thr Gln Asn Trp Val Leu Gly Thr Asn Ala Tyr Ile Asn Tyr Asp Ser			
	835	840	845
ttc ctg ttc aac ggg aac tac ctg agc ctc cag cca gca tcc ggc ttc			2592
Phe Leu Phe Asn Gly Asn Tyr Leu Ser Leu Gln Pro Ala Ser Gly Phe			
	850	855	860
ttc acg agc tac gct tac cag aag atc gat gaa tcc acg ctt aag cct			2640
Phe Thr Ser Tyr Ala Tyr Gln Lys Ile Asp Glu Ser Thr Leu Lys Pro			
	865	870	875
tac acg cgc tac aag gtg tcc ggg ttc atc ggg cag tca aac cag gtt			2688
Tyr Thr Arg Tyr Lys Val Ser Gly Phe Ile Gly Gln Ser Asn Gln Val			
	885	890	895
gaa ctg atc atc agc cgc tac ggg aag gaa atc gat aag atc ctt aac			2736
Glu Leu Ile Ile Ser Arg Tyr Gly Lys Glu Ile Asp Lys Ile Leu Asn			
	900	905	910
gtg cca tac gca ggg cca ctc cca atc acc gca gat gca agc atc acc			2784
Val Pro Tyr Ala Gly Pro Leu Pro Ile Thr Ala Asp Ala Ser Ile Thr			

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915	920	925	
tgc tgc gct cca gaa ata ggg cag tgc gat ggg gaa cag tca gat tcc Cys Cys Ala Pro Glu Ile Gly Gln Cys Asp Gly Glu Gln Ser Asp Ser 930 935 940			2832
cat ttc ttc aac tac agc atc gat gtt ggc gca ctc cat cca gaa ctt His Phe Phe Asn Tyr Ser Ile Asp Val Gly Ala Leu His Pro Glu Leu 945 950 955 960			2880
aac cca ggg atc gaa atc ggg ctg aag atc gtt cag agc aac ggc tac Asn Pro Gly Ile Glu Ile Gly Leu Lys Ile Val Gln Ser Asn Gly Tyr 965 970 975			2928
atc acc atc tcc aac ctt gaa atc atc gaa gaa aga cca tta acg gaa Ile Thr Ile Ser Asn Leu Glu Ile Ile Glu Glu Arg Pro Leu Thr Glu 980 985 990			2976
atg gaa att caa gca gtg aac cgc aag aac cag aag tgg gaa cgc gaa Met Glu Ile Gln Ala Val Asn Arg Lys Asn Gln Lys Trp Glu Arg Glu 995 1000 1005			3024
aag ctg ctt gaa tgc gca tcc atc tcc gaa ctc ctc cag cct atc atc Lys Leu Leu Glu Cys Ala Ser Ile Ser Glu Leu Leu Gln Pro Ile Ile 1010 1015 1020			3072
aac cag ata gat agc ctc ttc aag gat ggc aac tgg tac aac gat atc Asn Gln Ile Asp Ser Leu Phe Lys Asp Gly Asn Trp Tyr Asn Asp Ile 1025 1030 1035 1040			3120
cta cca cat gtt acc tac cag gat ctt aag aac atc atc atc cca gaa Leu Pro His Val Thr Tyr Gln Asp Leu Lys Asn Ile Ile Ile Pro Glu 1045 1050 1055			3168
ctt cct aag ctc aag cat tgg ttc atc gaa aac ctg cct ggg gaa tac Leu Pro Lys Leu Lys His Trp Phe Ile Glu Asn Leu Pro Gly Glu Tyr 1060 1065 1070			3216
cat gaa atc gaa cag aag atg aag gaa gca tta aag tac gca ttc act His Glu Ile Glu Gln Lys Met Lys Glu Ala Leu Lys Tyr Ala Phe Thr 1075 1080 1085			3264
cag ctc gat gaa aag aac ctg atc cat aac ggc cat ttc acc acc aac Gln Leu Asp Glu Lys Asn Leu Ile His Asn Gly His Phe Thr Thr Asn 1090 1095 1100			3312
ctc atc gat tgg cag gtg gaa ggc gat gct cag atg aag gtg ctt gaa Leu Ile Asp Trp Gln Val Glu Gly Asp Ala Gln Met Lys Val Leu Glu 1105 1110 1115 1120			3360
aac gat gca ctc gct ctc cag cta ttc aac tgg gat gct tcc gca tcc Asn Asp Ala Leu Ala Leu Gln Leu Phe Asn Trp Asp Ala Ser Ala Ser 1125 1130 1135			3408
cag agc atc aac atc cta gag ttc gat gaa gat aag gct tac aag ctg Gln Ser Ile Asn Ile Leu Glu Phe Asp Glu Asp Lys Ala Tyr Lys Leu 1140 1145 1150			3456
cgt gtg tac gca cag ggc tcc ggg acg atc cag ttc ggc aac tgc gaa Arg Val Tyr Ala Gln Gly Ser Gly Thr Ile Gln Phe Gly Asn Cys Glu 1155 1160 1165			3504
gat gaa gct atc cag ttc aac acc aac tca ttc atc tac cag gaa aag Asp Glu Ala Ile Gln Phe Asn Thr Asn Ser Phe Ile Tyr Gln Glu Lys 1170 1175 1180			3552
ata gtg tac ttc gat acg cca tcc gtt aac ctt cat atc cag agc gaa Ile Val Tyr Phe Asp Thr Pro Ser Val Asn Leu His Ile Gln Ser Glu 1185 1190 1195 1200			3600
ggc tcc gag ttc atc gtg agc agc atc gat ctc atc gaa ctc agc gat Gly Ser Glu Phe Ile Val Ser Ser Ile Asp Leu Ile Glu Leu Ser Asp 1205 1210 1215			3648
gat cag tag Asp Gln *			3657

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<210> SEQ ID NO 38
<211> LENGTH: 1218
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: APOSYNAXMI-031(FL)

<400> SEQUENCE: 38
Met Gln Ile Leu Gly Tyr Ser Ser Phe Val Ala Ile Ala Leu Leu Met
1 5 10 15
Ser Val Val Val Val Cys Asn Gly Gly Lys Thr Ser Thr Tyr Val Arg
20 25 30
Asn Leu Asp Cys Asn Leu Gln Ser Gln Gln Asn Ile Pro Tyr Asn Val
35 40 45
Leu Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly
50 55 60
Asp Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser
65 70 75 80
Leu Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe
85 90 95
Asn Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe
100 105 110
Val Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly
115 120 125
Trp Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile
130 135 140
Asn Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu
145 150 155 160
Asp Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp
165 170 175
Ser Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly
180 185 190
Thr Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp
195 200 205
Tyr Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala
210 215 220
Asn Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala
225 230 235 240
Pro Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser
245 250 255
Tyr Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp
260 265 270
Ala Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn
275 280 285
Met Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe
290 295 300
Lys Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val
305 310 315 320
Asp Thr Tyr Asn Val Tyr Ile Lys Gly Met Thr Leu Asn Val Leu Asp
325 330 335
Ile Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln
340 345 350

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Thr	Ala	Leu	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln
	355						360					365			
Glu	Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser
	370					375					380				
Phe	Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile
385					390					395					400
Ser	Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr
			405						410					415	
Pro	Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu
		420						425					430		
Asn	Tyr	Ala	Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu
	435					440						445			
Ser	Leu	Gly	Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn
	450					455					460				
Ala	Ala	Thr	Gln	Asn	Ser	Lys	Tyr	Leu	Asp	Gly	Glu	Ile	Leu	Asn	Gly
465					470					475					480
Ile	Gly	Ala	Ser	Leu	Pro	Gly	Tyr	Cys	Thr	Thr	Gly	Cys	Ser	Pro	Thr
			485					490						495	
Glu	Pro	Pro	Phe	Ser	Cys	Thr	Ser	Thr	Ala	Asn	Gly	Tyr	Lys	Ala	Ser
		500						505					510		
Cys	Asn	Pro	Ser	Asp	Thr	Asn	Gln	Lys	Ile	Asn	Ala	Leu	Tyr	Pro	Phe
	515					520						525			
Thr	Gln	Ala	Asn	Val	Lys	Gly	Asn	Thr	Gly	Lys	Leu	Gly	Val	Leu	Ala
	530					535					540				
Ser	Leu	Val	Ser	Tyr	Asp	Leu	Asn	Pro	Lys	Asn	Val	Phe	Gly	Glu	Leu
545					550					555					560
Asp	Ser	Asp	Thr	Asn	Asn	Val	Ile	Leu	Lys	Gly	Ile	Pro	Ala	Glu	Lys
			565					570						575	
Gly	Tyr	Phe	Pro	Asn	Asn	Ala	Arg	Pro	Thr	Val	Val	Lys	Glu	Trp	Ile
		580					585						590		
Asn	Gly	Ala	Ser	Ala	Val	Pro	Leu	Asp	Ser	Gly	Asn	Thr	Leu	Phe	Met
	595					600					605				
Thr	Ala	Thr	Asn	Leu	Thr	Ala	Thr	Gln	Tyr	Arg	Ile	Arg	Ile	Arg	Tyr
	610					615					620				
Ala	Asn	Pro	Asn	Ser	Asn	Thr	Gln	Ile	Gly	Val	Arg	Ile	Thr	Gln	Asn
625					630					635					640
Gly	Ser	Leu	Ile	Ser	Ser	Ser	Asn	Leu	Thr	Leu	Tyr	Ser	Thr	Thr	Asp
			645					650						655	
Met	Asn	Asn	Thr	Leu	Pro	Leu	Asn	Val	Tyr	Val	Ile	Gly	Glu	Asn	Gly
	660						665						670		
Asn	Tyr	Thr	Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr
	675					680					685				
Gly	Asp	Ile	Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile
	690					695					700				
Asp	Arg	Ile	Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn	Thr	Asn
705					710					715					720
Asn	Asn	Asn	Gly	Asn	Asn	Asn	Gly	Asn	Asn	Asn	Pro	Pro	His	His	Val
			725					730					735		
Cys	Ala	Ile	Ala	Gly	Thr	Gln	Gln	Ser	Cys	Ser	Gly	Pro	Pro	Lys	Phe
	740							745					750		

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Glu	Gln	Val	Ser	Asp	Leu	Glu	Lys	Ile	Thr	Thr	Gln	Val	Tyr	Met	Leu
		755					760					765			
Phe	Lys	Ser	Ser	Pro	Tyr	Glu	Glu	Leu	Ala	Leu	Glu	Val	Ser	Ser	Tyr
	770					775					780				
Gln	Ile	Ser	Gln	Val	Ala	Leu	Lys	Val	Met	Ala	Leu	Ser	Asp	Glu	Leu
785					790					795					800
Phe	Cys	Glu	Glu	Lys	Asn	Val	Leu	Arg	Lys	Leu	Val	Asn	Lys	Ala	Lys
				805					810					815	
Gln	Leu	Leu	Glu	Ala	Ser	Asn	Leu	Leu	Val	Gly	Gly	Asn	Phe	Glu	Thr
			820					825					830		
Thr	Gln	Asn	Trp	Val	Leu	Gly	Thr	Asn	Ala	Tyr	Ile	Asn	Tyr	Asp	Ser
		835					840					845			
Phe	Leu	Phe	Asn	Gly	Asn	Tyr	Leu	Ser	Leu	Gln	Pro	Ala	Ser	Gly	Phe
	850					855					860				
Phe	Thr	Ser	Tyr	Ala	Tyr	Gln	Lys	Ile	Asp	Glu	Ser	Thr	Leu	Lys	Pro
865					870					875					880
Tyr	Thr	Arg	Tyr	Lys	Val	Ser	Gly	Phe	Ile	Gly	Gln	Ser	Asn	Gln	Val
				885					890					895	
Glu	Leu	Ile	Ile	Ser	Arg	Tyr	Gly	Lys	Glu	Ile	Asp	Lys	Ile	Leu	Asn
			900					905					910		
Val	Pro	Tyr	Ala	Gly	Pro	Leu	Pro	Ile	Thr	Ala	Asp	Ala	Ser	Ile	Thr
		915					920					925			
Cys	Cys	Ala	Pro	Glu	Ile	Gly	Gln	Cys	Asp	Gly	Glu	Gln	Ser	Asp	Ser
	930					935					940				
His	Phe	Phe	Asn	Tyr	Ser	Ile	Asp	Val	Gly	Ala	Leu	His	Pro	Glu	Leu
945					950					955					960
Asn	Pro	Gly	Ile	Glu	Ile	Gly	Leu	Lys	Ile	Val	Gln	Ser	Asn	Gly	Tyr
				965					970					975	
Ile	Thr	Ile	Ser	Asn	Leu	Glu	Ile	Ile	Glu	Glu	Arg	Pro	Leu	Thr	Glu
			980				985						990		
Met	Glu	Ile	Gln	Ala	Val	Asn	Arg	Lys	Asn	Gln	Lys	Trp	Glu	Arg	Glu
	995						1000						1005		
Lys	Leu	Leu	Glu	Cys	Ala	Ser	Ile	Ser	Glu	Leu	Leu	Gln	Pro	Ile	Ile
	1010						1015					1020			
Asn	Gln	Ile	Asp	Ser	Leu	Phe	Lys	Asp	Gly	Asn	Trp	Tyr	Asn	Asp	Ile
1025					1030					1035					1040
Leu	Pro	His	Val	Thr	Tyr	Gln	Asp	Leu	Lys	Asn	Ile	Ile	Ile	Pro	Glu
				1045					1050					1055	
Leu	Pro	Lys	Leu	Lys	His	Trp	Phe	Ile	Glu	Asn	Leu	Pro	Gly	Glu	Tyr
		1060					1065							1070	
His	Glu	Ile	Glu	Gln	Lys	Met	Lys	Glu	Ala	Leu	Lys	Tyr	Ala	Phe	Thr
	1075					1080						1085			
Gln	Leu	Asp	Glu	Lys	Asn	Leu	Ile	His	Asn	Gly	His	Phe	Thr	Thr	Asn
	1090					1095					1100				
Leu	Ile	Asp	Trp	Gln	Val	Glu	Gly	Asp	Ala	Gln	Met	Lys	Val	Leu	Glu
1105					1110					1115					1120
Asn	Asp	Ala	Leu	Ala	Leu	Gln	Leu	Phe	Asn	Trp	Asp	Ala	Ser	Ala	Ser
				1125					1130					1135	
Gln	Ser	Ile	Asn	Ile	Leu	Glu	Phe	Asp	Glu	Asp	Lys	Ala	Tyr	Lys	Leu
			1140				1145						1150		
Arg	Val	Tyr	Ala	Gln	Gly	Ser	Gly	Thr	Ile	Gln	Phe	Gly	Asn	Cys	Glu

-continued

1155	1160	1165
Asp Glu Ala Ile Gln Phe Asn Thr Asn Ser Phe Ile Tyr Gln Glu Lys		
1170	1175	1180
Ile Val Tyr Phe Asp Thr Pro Ser Val Asn Leu His Ile Gln Ser Glu		
1185	1190	1195
Gly Ser Glu Phe Ile Val Ser Ser Ile Asp Leu Ile Glu Leu Ser Asp		
1205	1210	1215
Asp Gln		

That which is claimed:

1. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

- a) the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37, or a complement thereof;
- b) a nucleotide sequence having at least 90% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37, or a complement thereof;
- c) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38;
- d) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38; and,
- e) the delta endotoxin nucleotide sequence of the DNA insert of the plasmid deposited as Accession Nos. B-30935, B-30936, B-30937, or B-50046, or a complement thereof.

2. The isolated nucleic acid molecule of claim 1, wherein said nucleotide sequence is a synthetic sequence that has been designed for expression in a plant.

3. A vector comprising the nucleic acid molecule of claim 1.

4. The vector of claim 3, further comprising a nucleic acid molecule encoding a heterologous polypeptide.

5. A host cell that contains the vector of claim 3.

6. The host cell of claim 5 that is a bacterial host cell.

7. The host cell of claim 5 that is a plant cell.

8. A transgenic plant comprising the host cell of claim 7.

9. The transgenic plant of claim 8, wherein said plant is selected from the group consisting of maize, sorghum, wheat, cabbage, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, and oilseed rape.

10. A transgenic seed comprising the nucleic acid molecule of claim 1.

11. An isolated polypeptide with pesticidal activity, selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38;

- b) a polypeptide comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38;

- c) a polypeptide that is encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37;

- d) a polypeptide that is encoded by a nucleotide sequence that is at least 90% identical to the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37; and,

- e) a polypeptide encoded by the delta endotoxin nucleotide sequence of the DNA insert of the plasmid deposited as Accession Nos. B-30935, B-30936, B-30937, or B-50046.

12. The polypeptide of claim 11 further comprising heterologous amino acid sequences.

13. An antibody that selectively binds to the polypeptide of claim 11.

14. A composition comprising the polypeptide of claim 11.

15. The composition of claim 14, wherein said composition is selected from the group consisting of a powder, dust, pellet, granule, spray, emulsion, colloid, and solution.

16. The composition of claim 14, wherein said composition is prepared by desiccation, lyophilization, homogenization, extraction, filtration, centrifugation, sedimentation, or concentration of a culture of *Bacillus thuringiensis* cells.

17. The composition of claim 14, comprising from about 1% to about 99% by weight of said polypeptide.

18. A method for controlling a lepidopteran or coleopteran pest population comprising contacting said population with a pesticidally-effective amount of the polypeptide of claim 11.

19. A method for killing a lepidopteran or coleopteran pest, comprising contacting said pest with, or feeding to said pest, a pesticidally-effective amount of the polypeptide of claim 11.

20. A method for producing a polypeptide with pesticidal activity, comprising culturing the host cell of claim 4 under conditions in which the nucleic acid molecule encoding the polypeptide is expressed.

21. A plant having stably incorporated into its genome a DNA construct comprising a nucleotide sequence that encodes a protein having pesticidal activity, wherein said nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37;
- b) a nucleotide sequence having at least 90% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37;
- c) a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38;
- d) a nucleotide sequence encoding a polypeptide having at least 90% amino acid sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38; and,
- e) the delta endotoxin nucleotide sequence of the DNA insert of the plasmid deposited as Accession Nos. B-30935, B-30936, B-30937, B-50046, or a complement thereof,

wherein said nucleotide sequence is operably linked to a promoter that drives expression of a coding sequence in a plant cell.

22. The plant of claim 21, wherein said plant is a plant cell.

23. A method for protecting a plant from a pest, comprising introducing into said plant or cell thereof at least one expression vector comprising a nucleotide sequence that encodes a pesticidal polypeptide, wherein said nucleotide sequence is selected from the group consisting of:

- a) the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37;
- b) a nucleotide sequence having at least 90% sequence identity to the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37;
- c) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38;
- d) a nucleotide sequence that encodes a polypeptide having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38; and,
- e) the delta endotoxin nucleotide sequence of the DNA insert of the plasmid deposited as Accession Nos. B-30935, B-30936, B-30937, or B-50046, or a complement thereof.

24. The method of claim 23, wherein said plant produces a pesticidal polypeptide having pesticidal activity against a lepidopteran or coleopteran pest.

25. A method for protecting a plant from a nematode pest, comprising:

- a) introducing into said plant or cell thereof at least one expression vector comprising a nucleotide sequence that encodes a pesticidal polypeptide, wherein said pesticidal polypeptide has a molecular size greater than 22 kDa; and,

- b) growing said plant in a field containing cyst nematodes

26. The method of claim 25, wherein said cyst nematode is *Heterodera sp.*

27. The method of claim 26, wherein said cyst nematode is *Heterodera schachtii*.

28. The method of claim 25, wherein said pesticidal polypeptide is greater than about 40 kDa.

29. The method of claim 28, wherein said pesticidal polypeptide is greater than about 70 kDa.

30. The method of claim 29, wherein said polypeptide is selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38;
- b) a polypeptide comprising an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, or 38;
- c) a polypeptide that is encoded by the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37;
- d) a polypeptide that is encoded by a nucleotide sequence that is at least 90% identical to the nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 37; and,
- e) a polypeptide encoded by the delta endotoxin nucleotide sequence of the DNA insert of the plasmid deposited as Accession No. B-30935, B-30936, B-30937, or B-50046, or a complement thereof.

31. The method of claim 25, wherein said plant has an increased yield compared to a plant not expressing a nucleotide sequence encoding a pesticidal protein.

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